

351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKGLTGS  
401 SVTSLHAKTF IVDGKRIFIG SFNLDPRSAR LNTEMGVVIE SPKIAEOMER  
451 TLADTSPEYA YRVTLDRHNR LQWHDPATRK TYPNEPEAKL WKRIAALKLS  
501 LLPIESLL-

m987/a987 98.8% identity in 508 aa overlap

	10	20	30	40	50	60
m987.pep	MKTRSLISLLC <del>LLC</del> CS <del>SS</del> WL <del>PP</del> ER <del>TE</del> S <del>R</del> H <del>F</del> N <del>T</del> S <del>K</del> P <del>V</del> R <del>D</del> N <del>I</del> L <del>Q</del> I <del>R</del> H <del>P</del> T <del>H</del> N <del>G</del> L <del>S</del> D <del>I</del> Y					
a987	MKTRSLISLLC <del>LLC</del> CS <del>SS</del> WL <del>PP</del> ER <del>TE</del> S <del>R</del> H <del>F</del> N <del>T</del> S <del>K</del> P <del>V</del> R <del>D</del> N <del>I</del> L <del>Q</del> I <del>R</del> H <del>P</del> T <del>H</del> N <del>G</del> L <del>S</del> D <del>I</del> Y	10	20	30	40	50
m987.pep	LLNDPHEAFAARAALIESAEHSDLQ <del>Y</del> YIWRNDISGR <del>L</del> FLN <del>V</del> L <del>A</del> ERG <del>V</del> R <del>V</del> R <del>L</del> L <del>D</del> DN	70	80	90	100	110
a987	LLNDPHEAFAARAALIESAEHSDLQ <del>Y</del> YIWRNDISGR <del>L</del> FLN <del>V</del> L <del>A</del> ERG <del>V</del> R <del>V</del> R <del>L</del> L <del>D</del> DN	70	80	90	100	110
m987.pep	NTRGL <del>D</del> LLL <del>L</del> AL <del>D</del> SH <del>P</del> N <del>I</del> E <del>V</del> R <del>L</del> F <del>N</del> P <del>V</del> L <del>R</del> K <del>W</del> R <del>A</del> G <del>L</del> Y <del>T</del> D <del>F</del> P <del>R</del> L <del>N</del> R <del>R</del> M <del>H</del> N <del>K</del> S <del>F</del> T <del>A</del> D <del>N</del> R <del>I</del>	130	140	150	160	170
a987	NTRGL <del>D</del> LLL <del>L</del> AL <del>D</del> SH <del>P</del> N <del>I</del> E <del>V</del> R <del>L</del> F <del>N</del> P <del>V</del> L <del>R</del> K <del>W</del> R <del>A</del> G <del>L</del> Y <del>T</del> D <del>F</del> P <del>R</del> L <del>N</del> R <del>R</del> M <del>H</del> N <del>K</del> S <del>F</del> T <del>A</del> D <del>N</del> R <del>I</del>	130	140	150	160	170
m987.pep	LGGRNIGDEYFKVGED <del>T</del> V <del>F</del> AD <del>L</del> D <del>I</del> L <del>A</del> T <del>G</del> S <del>V</del> V <del>G</del> E <del>V</del> S <del>H</del> D <del>F</del> D <del>R</del> Y <del>W</del> A <del>S</del> H <del>A</del> N <del>T</del> R <del>I</del> I <del>R</del> S <del>G</del> D <del>I</del> G	190	200	210	220	230
a987	LGGRNIGDEYFKVGED <del>T</del> V <del>F</del> AD <del>L</del> D <del>I</del> L <del>A</del> T <del>G</del> S <del>V</del> V <del>G</del> E <del>V</del> S <del>H</del> D <del>F</del> D <del>R</del> Y <del>W</del> A <del>S</del> H <del>A</del> N <del>T</del> R <del>I</del> I <del>R</del> S <del>G</del> N <del>I</del> G	190	200	210	220	230
m987.pep	KGLQALGYN <del>D</del> E <del>T</del> S <del>R</del> H <del>A</del> L <del>R</del> R <del>Y</del> R <del>E</del> T <del>V</del> E <del>Q</del> S <del>P</del> L <del>Y</del> Q <del>K</del> I <del>Q</del> T <del>G</del> C <del>I</del> D <del>W</del> Q <del>S</del> V <del>R</del> T <del>R</del> L <del>I</del> S <del>D</del> D <del>P</del> A <del>K</del> G <del>L</del> R <del>D</del> R <del>R</del>	250	260	270	280	290
a987	KGLQALGYN <del>D</del> E <del>T</del> S <del>R</del> H <del>A</del> L <del>R</del> R <del>Y</del> R <del>E</del> T <del>V</del> E <del>Q</del> S <del>P</del> L <del>Y</del> Q <del>K</del> I <del>Q</del> T <del>G</del> R <del>I</del> D <del>W</del> Q <del>S</del> V <del>Q</del> T <del>R</del> L <del>I</del> S <del>D</del> D <del>P</del> A <del>K</del> G <del>L</del> R <del>D</del> R <del>R</del>	250	260	270	280	290
m987.pep	RK <del>P</del> PIA <del>G</del> R <del>L</del> Q <del>D</del> A <del>L</del> K <del>Q</del> P <del>E</del> K <del>S</del> V <del>Y</del> L <del>V</del> S <del>P</del> Y <del>F</del> V <del>P</del> T <del>K</del> S <del>G</del> T <del>D</del> A <del>L</del> K <del>V</del> Q <del>D</del> G <del>I</del> D <del>V</del> T <del>V</del> L <del>T</del> N <del>S</del> L <del>Q</del> A <del>T</del> D <del>V</del> A	310	320	330	340	350
a987	RK <del>P</del> PIA <del>G</del> R <del>L</del> Q <del>D</del> A <del>L</del> K <del>Q</del> P <del>E</del> K <del>S</del> V <del>Y</del> L <del>V</del> S <del>P</del> Y <del>F</del> V <del>P</del> T <del>K</del> S <del>G</del> T <del>D</del> A <del>L</del> K <del>V</del> Q <del>D</del> G <del>I</del> D <del>V</del> T <del>V</del> L <del>T</del> N <del>S</del> L <del>Q</del> A <del>T</del> D <del>V</del> A	310	320	330	340	350
m987.pep	AVHSGYV <del>K</del> YR <del>K</del> P <del>L</del> L <del>K</del> A <del>G</del> I <del>K</del> L <del>Y</del> E <del>L</del> Q <del>P</del> N <del>H</del> A <del>V</del> P <del>A</del> T <del>K</del> D <del>G</del> L <del>T</del> G <del>S</del> S <del>V</del> T <del>S</del> L <del>H</del> A <del>K</del> T <del>F</del> I <del>V</del> D <del>G</del> K <del>R</del> I <del>F</del> G	370	380	390	400	410
a987	AVHSGYV <del>K</del> YR <del>K</del> P <del>L</del> L <del>K</del> A <del>G</del> I <del>K</del> L <del>Y</del> E <del>L</del> Q <del>P</del> N <del>H</del> A <del>V</del> P <del>A</del> T <del>K</del> D <del>G</del> L <del>T</del> G <del>S</del> S <del>V</del> T <del>S</del> L <del>H</del> A <del>K</del> T <del>F</del> I <del>V</del> D <del>G</del> K <del>R</del> I <del>F</del> G	370	380	390	400	410
m987.pep	S <del>F</del> N <del>L</del> D <del>P</del> R <del>S</del> A <del>R</del> L <del>N</del> T <del>E</del> M <del>G</del> V <del>V</del> I <del>E</del> S <del>P</del> K <del>I</del> A <del>E</del> Q <del>M</del> E <del>R</del> T <del>L</del> A <del>D</del> T <del>T</del> P <del>A</del> Y <del>A</del> R <del>V</del> T <del>L</del> D <del>R</del> H <del>N</del> R <del>L</del> Q <del>W</del> H <del>D</del> P <del>A</del> R <del>K</del>	430	440	450	460	470
a987	S <del>F</del> N <del>L</del> D <del>P</del> R <del>S</del> A <del>R</del> L <del>N</del> T <del>E</del> M <del>G</del> V <del>V</del> I <del>E</del> S <del>P</del> K <del>I</del> A <del>E</del> Q <del>M</del> E <del>R</del> T <del>L</del> A <del>D</del> T <del>S</del> P <del>E</del> Y <del>A</del> R <del>V</del> T <del>L</del> D <del>R</del> H <del>N</del> R <del>L</del> Q <del>W</del> H <del>D</del> P <del>A</del> R <del>K</del>	430	440	450	460	470
m987.pep	T <del>Y</del> P <del>N</del> E <del>P</del> A <del>E</del> K <del>L</del> W <del>K</del> R <del>I</del> A <del>A</del> K <del>I</del> L <del>S</del> L <del>L</del> P <del>I</del> E <del>G</del> L <del>L</del> X	490	500	509		
a987	T <del>Y</del> P <del>N</del> E <del>P</del> A <del>E</del> K <del>L</del> W <del>K</del> R <del>I</del> A <del>A</del> K <del>I</del> L <del>S</del> L <del>L</del> P <del>I</del> E <del>G</del> L <del>L</del> X	490	500			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEO ID 2979>:

9988, seq.

1 ATGAATAAAA ATATTAATC TTTAAATTG CGGGAAAAAG ACCCGTTTTT

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51  AAGTCGTGAA AAACAGCGTT ATGAACATCC TTTGCCAGT CGGgaATGGA
101 TAATCGAATT GTTGGAGCGC AAAGGTGTGC CTTCAAAAAT CGAATCGCTT
151 GCACCGGAGC TGTCGATTAC GGAAGacgag tATGTCTTT TTGAACGCCG
201 TCTGAaggCG atgGCGCGGG AcggcAGGT TTTATCAAC CGCCgaggcg
251 CagtTTGCGc gGCggacaag ctgGATTGG TCAATGccg Cgtcgaggcg
301 catAAgAcg gtttcggctt cgcCGTCCGG CTCATGCCGA TGGAACGAGG
351 GGATTCGTT TTATACGAAC GCCAgatgcg tggTGTcatG CACggcgaca
401 ccgttACCGT CCGCCTCGCg ggtatggaaCC GCAGGGGccg ccgcGAAGgg
451 acgtttctGG ATATTGTCGA ACGCGCGAA AGCAAGTTG TCGGCGTGT
501 CTATATGGAT AGGGGCGTGG CGATTTGGA GCCGGAAGAC AAGCGCTCTGA
551 ACCAAAGCAT CGTGTGGAA CCGGACGGCG TGGCGCTTT CAAACCCGAA
601 TCCGGTCAGG TTATCGTCGG CAAAATTGAG GTTTATCCCG AGCAAAACCG
651 GCGTGCAGTG CAAAAAAATCA TTGAAGTTT GGGCGATTAT GCGGACAGCG
701 GGATGGAAAT cgAAATTGCG GTGCGCAAGC ATCATTGCG GCAccgaTTC
751 AGTGAAagcgt gtGcCAAATC CGcgaAAAA ATtcccgacc ATGTACGCAA
801 AAGCGATTG AAAGGCCGCG TCGATTGTTG CGACCTTCCT TTGGTAACGA
851 TAGACGGCGA AACGGCGCG GATTTGACG ACGCCGGTGT TGCGGAAAAAA
901 GTCGGACGCA ATTACCGCCT GGTGCGGCG ATTGCGGATG TCAGCCATT
951 TGTCGCCCT GACGATGCGA TTGATGCGA TGCTCAAGAA CGCAGTACCA
1001 GCGTGTATTG CCGCGCCCGT ATGATTCCGA TGCTGCCGGA AAACCTGTCC
1051 AACGGCATCT GCTCGCTCAA TCCCGATGTC GAGCCTTTGT GTATGGTGTG
1101 CGATATGGTC GTTACCTATG CGGGCAATAT CAA-GAATAC CGTTCTATC
1151 CGCCCGTGT GCGCTCTCAT GCCCCCTGAA CCA-GAAGTTGGAAA
1201 TGGCTTCAG ACGGCATCGG GAATCCGCAC AAAGGCCAAA TCGACACGCT
1251 TTACAAGCTG TTTAAATTT TGCAGAAAAA ACGTCGCG CGCGGGCGG
1301 TGGAGTTGA AAGCGTCGAA ACCCAGATGA TTTGACGAA CAACGGCAA
1351 ATCGAAAAAA TTGTCCCCGT CGTCCGCAAC gatGCCACA AGTGATTGA
1401 AGAATGTATG CTGGCGCGA ATGTTGCGC GGGGGATTTT CTGTGAAAA
1451 ACAAACATAC GCGCTTGTTC CGCAACCATT TGGGCCCCAC GCGGAAAAAA
1501 CTCGCCACCC TGCAGGAGCA GCTCGCTGTG TTGGGGCTTC AACTTGGCGG
1551 CGGGGACAAAC CCGTCGCCGA AAGACTATGC CGCGCTTGCC GAAACATTCA
1601 AAGGCAGGCC GGATGCGAA TTGCTGCAAG TCATGATGTT GCGCTCCATG
1651 CAGCAGGCCG TTTACGAACC GCATTGCGAA GGGCATTTCG GTTGGCTTA
1701 TGAAGCATAC GCCCCACTTAA CCTCGCCCAT CGCGCCTAT CCCGACCTGA
1751 CCGTCCACCG TGCCATCAA GCGTATTGA ACCGGAAAAC CTACACGCCA
1801 AACAAAAGCT GGCAGGCTTT GGGCGTGCAT ACTTCGTTT GCGAACGCCG
1851 TGCGCAGCAT GCTGGCGCG ATGTTGAAAAA CTGGCTGAAA ACTTATTATA
1901 TGCGCGATAA GGTGGTGAAT ATTTGAG GcaaattCtc cgggggtgtg
1951 gcaaatttgcgaaATATTGTCGACTTTGGAC GATATccata tcgacggct
2001 ggtacaTATC AGCAGtttgg gcgAGATTA TTTCaacttc cgccccgAAA
2051 TCATGGCAAT CGAAGGCAGA CGCAGCGCA TCCGTTCAA TATGGGGAC
2101 AGGGTTGCCG TCCGGGTCGC GCGTGGCGAT TTGGATGATG GAAAATCGA
2151 CTTTGTCTTA ATTGCCGGAG AAAGCGCGAG GCGGGCGGAAG GTCAAATTAT
2201 CCGCATCTGC CAAACCGGCA GGGGCGGGGG GGAAAGGGAA ATCGAAAACC
2251 ACCGCCGAGA AAAAACAGC CCGATGCCG AAAGTAAGGG GAAGGGCGT
2301 GCGTCCGTT GCGGAATCGG GGAAAAGGC AAAGAAACCG GTTCCGATTAA
2351 AGGTCAAAAAA ACGGAAAGGC AAATCATAA

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This corresponds to the amino acid sequence <SEQ ID 2980; ORF 988.ng>:

g988.pep

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1  MNKNIKSLNL REKDPFLSRE KQRYEHPLPS REWIIELLER KGVP SKIESL
51  ARELSITEDE YVFFERRLKA MARDQVILIN RRGAVCAADK LDIVKCRVEA
101 HKDGFGEFAVP LMPMDEGDFV LYERQMRGVM HGDVTVRPA GMDRRRRREG
151 TFLDIVERAQ SKVVRPFYMD RGVAILEPED KRLNQSIVLE PDGVARFKPE
201 SGQVIVGKVE VYPEQNRPV AKIIIEVLGDY ADSGMEIEIA VRKHHLPHRF
251 SEACAKSAKK IPDHVRKSDL KGRV DLDLDP LVTIDGETAR DFDDAVFAEK
301 VGRNYRLVVA IADVSHYVRP DDAIDADAQE RSTSVYFPRR MIPMLPENLS
351 NGICSLNPDV ERLCMVCDMV VTYAGNIKEY RFYPAVMRSH ARLTYNQVWK
401 WLSDGIGNPH KAQIDTLYKL FKILQKKRLA RGA VEFESVE TQMIFDDNGK
451 IEKIVPVVRN DAHKLIEECM LAANVCAADF LLKNKHTALF RNHLGPTPEK
501 LATLREQQLGL LGLQLGGGDN PSPKDYAALA EQFKGRPDAE LLOVMMRLSM
551 QQAVYEPHCE GHFGGLAYEAY AHFTSPIRRY PDLT VHRRAIK AVLNRKTYTP
601 NKSWOALGVH TSFCERRADD AGRDVENWLK TYYMRDKVGE IFEKGKISRGV
651 ANFGIFVTL DIIHDLVHI SDLGEDYFN RPEIMAIECF RSGIRFNMGD
701 RVAVRVARAD LDDGKIDFVL IAGESGRRRK VKLSASAKPA GAAGKGKSRT
751 TAEKKTARCG KVRGRGPVAV AESGKKAKKP VPIVKKRKG KS.

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2981>:

m988.seq	(partial)
1	..ACAGTTCTGG ATATTGTCGA ACGCGCGAA AGCAAAGTGG TCGGCCGTTT
51	CTATATGGAT AGGGCGTGG CGATTGGA GCGGAAGAC AAGCGTCTGA
101	ACCAAAGCAT CGTATTGAA CCGGACGGCG TGGCGCGTTT CAAACCTGAA
151	TCCGGTCAGG TCATCGTCGG CGAAATTGAG GTTATCCTG AGCAAAACCG
201	GCCGGCAGTG GCAAAAATCA TCGAAGTTTT GGGCGATTAT GCCGACAGCG
251	GCATGGAGAT TGAAATTGCG GTGCGCAAGC ATCATTGCG GCACCAATTG
301	AGTGAAGCGT GTGCAAAGC TCGAAAAAAA ATTCCCGTCC ATGTACGCAA
351	AAGCGATTG AAAGGCCGG TCGATTGCG CGACCTGCCT TTGTAACGA
401	TAGACGGCA AACGGCGC GATTTGAGC ACGCGGTGTT TGCCGAAAAAA
451	GTCGGACGCA ATTACCGTCT GGTCGTGGCG ATTGCGGATG TCAGCCATTA
501	TGTCCGCCCT GACGATGTGA TTGATGCAGA TGCTCAAGAA CGCAGTACCA
551	GCGTATATTG CCGCGCCGT GTGATTCCGA TGCTGCCGGA AAACCTGTCT
601	AACGGCATTT GCTCGCTAA TCCCAGATGTC GAGCGTTTGT STATGGTGTG
651	CGATATGCTC GTTACCTAT CGGGCAATAT CAAAGAATAC CGCTTCTACC
701	CCGCCGTAAT GCGCTCTCAT GCGCCCGTGA CCTACAACCA AGTTTGGAAA
751	TGGATTTAG ACGGCATCGA CCATCCGTAC AAAGCCAAA TCGACACCCCT
801	TTACAAACTC TTCAAAATCC TTCAGAAAAA GCGTTGAA CGCGGCGCG
851	TGGAGTTGA AAGCGTCGA ACCCAGATGA TTTCGATGA CAACGGCAAA
901	ATCGAAAAAA TCGTCCCCGT TGTCCGCAAC GATGCCACA AGCTGATTGA
951	AGAATGTATG CTGGCGCGA ATGTTGCGC AGCGGATTTC CTGTTGAAAA
1001	ACAAGCATAAC GGCTTTGTC CGCAACCAT TGGGCCAAC GCGGAAAAAA
1051	CTCGCCACCC TGCAGCGAGCA GCTCGGTCTG TTGGGCTTC AACTTGGCG
1101	CGGGGACAAAC CGTCGCCGA AAGACTATGC CGCGCTTGTG GAAATTCA
1151	AAGGCAGACC TGATGCCGA TTGCTGCAAG TCATGATGTT CGCGCCATG
1201	CAGCAGGCCG TTTACGAACC GCATTGCGAC GGACACTTTG STCTTGCCTA
1251	CGAAGCATAAC GCCCCACTTCA CCTCGCCCAT CGGGCGCTAT CCCGACCTGA
1301	CCGTACACCG CGCCATCAAA GCGTGTGTTGA ATCAGCAAAC CTACACGCCA
1351	AAAAAAAGCT GGCAGGCTT GGGCGTGCAT ACCTCGTTCT GTGAGCGCCG
1401	TGCGGACGAC GCCAGCCGCC ACGTGAAAAA CTGCGTGAAC ACCTATTATA
1451	TGCGCGATAAA GGTCGGCGAA GTATTGAG GTAAAATCTC CGGCATGACC
1501	AGTTTTGGTA TCTTTGTAAC ACTGGACGGC ATCCACATTG ACGGCTTGGT
1551	GCATATCAGC GATTGGCG AAGACTATTG CAACTTCCGC CCCGAAATCA
1601	TGGCAATCGA AGGCAGAACGC AGGCCATCC GTTCAACAT GGGGGACAGG
1651	GTTGCCGTCC GGGTCGCCCG TGCCGATTG GATGACGGAA AAATCGATT
1701	TGTCCCTGATT GCCGGGGGGG CGGGCAGGGG CGGAAAGTT AAATCATCCG
1751	CGTCTGCCAA ACCGGCAGGG ACGGCGGGGA AAGGAAAGCC GAAAACCGCC

1400

1801      GCCGAGAAAAA AAACAGCCCG AGGCAGCAAA GTAAGGGAA GGGGCGCGTC  
 1851      TGCCGCCGCA GAATCGAGGA AAAAGGCAAA GAAACCGGTT CCGATTAAGG  
 1901      TAAAAAAACG GAAAGGCAAA TCATAA

This corresponds to the amino acid sequence <SEQ ID 2982; ORF 988>:

m988.pep (partial)

1    ..TVLDIVERAQ SKVVGGRFYMD RGVAILEPED KRLNQSIVLE PDGVARFKPE  
 51    SGQVIVGEIE VYPEQNRPAV AKIIIEVLGDY ADSGMEIEIA VRKHHLPHQF  
 101    SEACAKAAKK I PVHVRKSDL KGRVDLRDLPLV TIDGETAR DFDDAVFAEK  
 151    VGRNYRLVVA IADVSHYVRP DDVIDADAQE RSTSVYFPRR VIPMLPENLS  
 201    NGICSLNPDV ERLCMVCDMV VTYAGNIKEY F F YPAVMRSW ARLTYNQVWK  
 251    WISDGIDH PY KA QIDTLYKL FKILOKKRFE RGAVEFESVE TQMIFDDNGK  
 301    IEKIVPVVRN DAHK I EECM LAANVCAADF LLKNKHTALF RNHLGPTPEK  
 351    LATLREQQLGL LGLQLGGDN PSPKDYAALV EQFKGRPDAE LLQVMMRLSM  
 401    QQAVYEPHCD GHFGLAYEAY AHFTSPIRR PDLTVHRAIK AVLNQQTYTP  
 451    KKSQWALGVH TSFCERRADD ASRDVENWLK TYYMRDKVGE VFEKGKISGMMT  
 501    SFGIFVTLDG IHIDGLVHIS DLGEDYFNFR PEIMAI EGER SGIRFNMGDR  
 551    VAVRVARADL DDGKIDFVLI AGGSGRGRKV KSSASAKPAG TAGKGKPKTA  
 601    AEKKTARGGK VRGRGASAAA ESRKKAKKPV PIKVKKRKGK S \*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m988/g988 94.2% identity in 642 aa overlap

	10	20	30			
m988.pep	TVLDIVERAQSKVVGGRFYMDRGVAILEPED					
g988	LYERQMRGVHMHGDTVTVRPAGMDRRGRREGTFLDIVERAQSKVVGGRFYMDRGVAILEPED	130	140	150	160	170
						180
	40	50	60	70	80	90
m988.pep	KRLNQSIVLEPDGVARFKPESGQVIVGEIEVYYPEQNRPAVAKIIEVLGDYADSGMEIEIA					
g988	KRLNQSIVLEPDGVARFKPESGQVIVGKIEVYYPEQNRPAVAKIIEVLGDYADSGMEIEIA	190	200	210	220	230
						240
	100	110	120	130	140	150
m988.pep	VRKHHLPHQFSEACAKAAKK I PVHVRKSDLKGRVDLRDLPLV TIDGETARDFDDAVFAEK					
g988	VRKHHLPHRFSEACAKSAAKK I PDHVRKSDLKGRVDLCDLPLV TIDGETARDFDDAVFAEK	250	260	270	280	290
						300
	160	170	180	190	200	210
m988.pep	VGRNYRLVVAIADVSHYVRPDDVIDADAQE RSTSVYFPRR VIPMLPENLSNGICSLNPDV					
g988	VGRNYRLVVAIADVSHYVRPDDAIDADAQE RSTSVYFPRRM VIPMLPENLSNGICSLNPDV	310	320	330	340	350
						360
	220	230	240	250	260	270
m988.pep	ERLCMVCDMV VTYAGNIKEYRFYPAVMRSW ARLTYNQVWK WISDGIDH PY KA QIDTLYKL					
g988	ERLCMVCDMV VTYAGNIKEYRFYPAVMRSW ARLTYNQVWK WISDGIDH PY KA QIDTLYKL	370	380	390	400	410
						420
	280	290	300	310	320	330
m988.pep	FKILOKKRFERGAVEFESVETQMIFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF					
g988	FKILOKKRFERGAVEFESVETQMIFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF	430	440	450	460	470
						480
	340	350	360	370	380	390
m988.pep	LLKNKHTALFRNHLGPTPEK LATLREQLGLLGLQLGGDNPSPKDYAALVEQFKGRPDAE					
g988	LLKNKHTALFRNHLGPTPEK LATLREQLGLLGLQLGGDNPSPKDYA FKGRPDAE					

	490	500	510	520	530	540
	400	410	420	430	440	450
m988 . pep	LLQVMMRLSRSMQQAVYEPHCDGHFGLAYEAYAHFTSPIRYPDLTVHRAIKAVLNQQTYP					
g988	:     :     :     :     :     :     :     :     :     :					
	550	560	570	580	590	600
	460	470	480	490	500	509
m988 . pep	KKSWQALGVHTSFCERRADDASRDVENWLKTYYMRDKVGEVFEKGKIS-GMTSFGIFVTLD					
g988	:     :     :     :     :     :     :     :     :     :					
	610	620	630	640	650	660
	510	520	530	540	550	560
m988 . pep	GIHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRFNMGDRVAVRVARADLDDGKIDFVL					
g988	:     :     :     :     :     :     :     :     :					
	670	680	690	700	710	720
	570	580	590	600	610	620
m988 . pep	IAGGSGRGRKVKSASAKPAGTAGKGPKTAEEKKTARGGKVRGRGASAAAESRKKA					
g988	:     :     :     :     :     :     :     :     :					
	730	740	750	760	770	780
	630	640				
m988 . pep	VPIKVKKRKGSX					
g988	:					
		VPIKVKKRKGSX				
		790				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2983>:

a988 . seq	1	ATGAATAAAA ATATTAAATC TTTAAATTAA CGGGAAAAAG ACCCGTTTT
	51	AACTCGTGAA AAACAGCGTT ATGAACATCC TTTGCCAGT CGGAAATGGA
	101	TAATCGAGCT GCTTGAACGT AAAGGCGTAC CATCCAAGAT TGAAGCTTTG
	151	GTACCGAAT TGTCGATTA GGAAGAAGAG TACGAATTT TCGAACGTG
	201	TCTGAAGGCG ATGGCCGGG ACGGTCAAGT TTTAATCAAC CGTCGGGGCG
	251	CGGTTGCGC CGGCCACAAA TTGGATTGG TCAAATGCCG TGCAAGGCCG
	301	CACAAAGACC GCTTCGGTT CGCCGTGCCG CTCACGCCG CCAAAGACGG
	351	TGATTGGTC TTGTACGAAC GCCAGATGCG CGGCATTATG CACGGCGATA
	401	TTGTCACTGT TCGTCTGCC GGCATGGACG GTAGGGGCC CGCGAAGGG
	451	ACGGTTCTGG ATATTGTCGA ACGCGCGAA AGCAAAGTGG TCGGCCGTT
	501	CTANATGGAT AGGGCGTGG CGATTGGAA GCGGAAGAC AAGCGTCTGA
	551	ACCAAAGCAT CGTATTGGAA CGGGACGGCG TGGCGCGTTT CAAACCTGAA
	601	TCCCGTCAGG TCATCGTCGG CGAAATTGAG GTTTATCCTG AGCAAACCG
	651	GCCGGCAGTG GCAAAATCA TCGAAGTTT GGGCGATTAT GCCGACAGCG
	701	GCATGGAGAT TGAAATTGCC GTGCGCAAGC ATCATTGCC GCACCAATTG
	751	AGTGAAGCGT GTGCCAACAG CGCGAAAAAA ATTCCCGACC ATGTACGCAA
	801	AAGCGATTG AAAGGCCGCG TCGATTGCG CGACCTGCCT TTGTTAACGAA
	851	TAGACGGCGA AACCGCTCGA GATTTGACG ATGCGGTGTT TGCCGAGAAA
	901	ATCGGACGCA ATTACCGTCT GGCGTGGCG ATTGCCGATG TCAGCCATTA
	951	TGTCCGCCCG GATGACCGCTA TCGACACCGA CGCTCAGGAA CGCAGCACCA
	1001	GTGTTTACTT CCGCGCCGC GTGATTCCA TGTTGCCGGA AAACCTGTCC
	1051	AACCGCATCT GCTCGCTCAA TCCTCATGTC GAGCCTTGT GTGTTGTGTG
	1101	CGATATGGTT ATCACTTACG CGGGCAATAT CAAAGAATAC CGCTTCTACC
	1151	CCGGCGTGAT GCGCTCTCAT GCGCGCTGA CCTACACCA AGTTGGAAA
	1201	TGGCTTCAG CGGGCATCGA GCATCCGTC AAAACCCAAA TCGACACGCT
	1251	TTACAAACTC TTCAAAATCC TTCAGAAAAA GCGTTTCGAA CGCGGGCGG
	1301	TGGAGTTGA CAGCATCGA ACCCAAATGC TTTTCGACGA CAACGGTAAA
	1351	ATTGAAAAAA TCGTCCCCGT TGTCCGCAAC GATGCCACAGCTGATTGA
	1401	AGAATGTATG TTGGCGGCAA ACGTTTGCGC AGCGGATTTT CTGTTGAAAAA
	1451	ACAAGCATAAC CGCATTGTC CGCAACCATT TGGGGCCAC GCCCGAAAAAA
	1501	CTCGCCGCT TCGCGAGCA GCTCGGTCTG TTGGGGCTTC AACTTGGCGG
	1551	CGGGCACAAC CGCTCGCCGA AAGACTATGC CGCGCTTGCC GGACAGTTCA

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1601 AAGGCAGGCC GGATGCCGAA TTGCTGCAAG TCATGATGTT GCGCTCCATG
1651 CAACAGGCCG TTTACGAACC GCATTGCGAC GGACACTTG GTCTTGCCTA
1701 CGAACATAC GCCCACTTC CCTCGCCCAT CCGCCGCTAT CCCGACCTGA
1751 CCGTACACCG CGCCATCAA GCCGTGTTGA ATCAGCAAAC CTACACGCCA
1801 AAAAAAAGCT GGCAGGCTTT GGGCGTCAT ACCTCGTTCT GTGAGCGCCG
1851 TGCCGACGAC CGCAGCCGCG ACCTGGAAA CTGGCTGAAA ACCTATTATA
1901 TGCGCGATAA GGTCGGCGAA GTATTCGAGG GTAAAATCTC CGGCATGACC
1951 AGTTTGGTA CTTTGTAAAC ACTGGACGGC ATCCACATTG ACGGCTTGGT
2001 GCATATCAGC GATTGGCGC AAGACTATT CAACTCCGC CCCGAAATCA
2051 TGGCAATCGA AGGCGAACGC AGCGGCATCC GTTTCACAT GGGGGACAGG
2101 GTTGCCTGTC GGGTCGCCCC TGCCGATTG GATGACGGAA AAATCGATT
2151 TGTCTGATT GCCGGGGGGA GCGGCAGGGG GCGGAAAGTT AAATCATCCG
2201 CGCTCTGCAA ACCGGCAGGG ACCGGCGGGGA AAGGGAAGCC GAAAACCGCC
2251 GCGGAGAAAA AAACAGCCCG AGGCGGCAAA GTAAGGGGAA GGGGCGCGTC
2301 TGCCGCGCA GAATCGAGGA AAAAGGCAAA GAAACCGGTT CCGATTAAAGG
2351 TAAAAAAACG GAAAGGCAAA TCATAA

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This corresponds to the amino acid sequence <SEQ ID 2984; ORF 988.a>:

```

a988.pep
 1 MNKNIKSLNL REKDPFLSRE KQRYEHPLPS REWIIELLER KGVPSKIEAL
 51 VRELSIKEEE YEFFERRLKA MARDQQLIN RRGAVCAADK LDIVKCRVKA
101 HKDRFGFAVP LTPAKDGFV LYERQMRGIM HDIVTVRPA GMDGRGRREG
151 TVLDIVERAQ SKVVGRCFXMD RGVAILEPED KRLNQSIVLE PDGVARFKPE
201 SGQVIVGEIE VYPEQNRPAY AKIIIEVLGDY ADSGMEIEIA VRKHHLPHQF
251 SEACAKAAK IPDHVRKSDL KGRVDLRDLPLV TIDGETAR DFDDAVFAEK
301 IGRNYRLVVA IADVSHYVRP DDAIDTDAQE RSTSVYFPYR VIPMLPENLS
351 NGICSLNPHV ERLCVVCDMV ITYAGNIKEY RFYPAVMRSH ARLTYNQVWK
401 WLSGGIEHPF KTQIDTLYKL FKILQKKRFE RGAVEFEDSIE TQMLFDDNGK
451 IEKIVPVVRN DAHKLIEECM LAANVCAADF LLKNKHTALF RNHLGPTPEK
501 LAALREQLGL LGLQLGGGDN PSPKDYAALA GQFKGRPDAE LLQVMMRLSM
551 QQAVYEPHCD GHFGLAYEAY AHFTSPIRRY PDLTVHRAIK AVLNQQTYTP
601 KKSWQALGVH TSFCERRADD ASRDVENWLK TYYMRDKVGE VFECKISGMT
651 SFGIFVTLGD IHIDGLVHIS DLGEDYFNFR PEIMAIIEGER SGIRFNMGDR
701 VAVRVARADL DDGKIDFVLI AGGSGRGRKVV KSSASAKPAG TAGKGKPKTA
751 AEKKTARGKK VRGRGASAAA ESRKKAKKPV PIKVKKRKKGK S*

```

m988/a988 97.0% identity in 641 aa overlap

		10	20	30			
m988.pep		TVLDIVERAQSKVVGRCFYMDRGVAILEPED					
a988	LYERQMRGIMHDIVTVRPAGMDGRGRREGTVLDIVERAQSKVVGRCFXMDRGVAILEPED	130	140	150	160	170	180
m988.pep	KRLNQSIVLEPDGVARFKPESGQVIVGELEVYYPEQNRPAYAKIIIEVLGDYADSGMEIEIA	40	50	60	70	80	90
a988	KRLNQSIVLEPDGVARFKPESGQVIVGEIEVYYPEQNRPAYAKIIIEVLGDYADSGMEIEIA	190	200	210	220	230	240
m988.pep	VRKHHLPHQFSEACAKAKIIPVHVRKSDLKGRVDLRDLPLVTIDGETARDFDDAVFAEK	100	110	120	130	140	150
a988	VRKHHLPHQFSEACAKAKIIPDHRVRKSDLKGRVDLRDLPLVTIDGETARDFDDAVFAEK	250	260	270	280	290	300
m988.pep	VGRNYRLVVAIADVSHYVRPDDVIDADAQERSTSVYFPYRIPMLPENLSNGICSLNPDV	160	170	180	190	200	210
a988	VGRNYRLVVAIADVSHYVRPDDAIDTDAQERSTSVYFPYRIPMLPENLSNGICSLNPDV	310	320	330	340	350	360
m988.pep	ERLCMVCMDMVVTYAGNIKEYRFYPAVMRSHARLTYNQVWKWISDGIDHPYKAQIDTLYKL	220	230	240	250	260	270
a988	ERLCVVCMDMVITYAGNIKEYRFYPAVMRSHARLTYNQVWKWLGGIEHPFKTQIDTLYKL						

1403

	370	380	390	400	410	420
m988 . pep	280	290	300	310	320	330
	FKILQKKRFERGAVEFESVETQMIFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF					
a988		FKILQKKRFERGAVEFDSIETQMLFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF				
		430	440	450	460	470
m988 . pep	340	350	360	370	380	390
	LLKNKHTALFRNHLGPTPEKLATLREQLGLLQLQGGDNPSPKDYAALVEQFKGRPDAE					
a988		LLKNKHTALFRNHLGPTPEKLAALREQLGLLQLQGGDNPSPKDYAALAGQFKGRPDAE				
		490	500	510	520	530
m988 . pep	400	410	420	430	440	450
	LLOVMMRLSRMQQAVYEPHCDGHFGLAYEAYAHFTSPIRYPDLTVHRAIKAVLNQQTYTP					
a988		LLQVMMRLSRMQQAVYEPHCDGHFGLAYEAYAHFTSPIRYPDLTVHRAIKAVLNQQTYTP				
		550	560	570	580	590
m988 . pep	460	470	480	490	500	510
	KKSWQALGVHTSF CERRADDASRDVENWLKTYYMRDKVGEVFEKGKISGMTSFGIFVTL DG					
a988		KKSWQALGVHTSF CERRADDASRDVENWLKTYYMRDKVGEVFEKGKISGMTSFGIFVTL DG				
		610	620	630	640	650
m988 . pep	520	530	540	550	560	570
	IHIDGLVHISDLGEDYFNRPEIMAIEGERSGIRFNMGDRVAVRVARADLDDGKIDFVLI					
a988		IHIDGLVHISDLGEDYFNRPEIMAIEGERSGIRFNMGDRVAVRVARADLDDGKIDFVLI				
		670	680	690	700	710
m988 . pep	580	590	600	610	620	630
	AGGSGRGRKVKS SAKPAGTAGKGKPKTAAEKKTARGKVRGRGASAAAESRKAKKPV					
a988		AGGSGRGRKVKS SAKPAGTAGKGKPKTAAEKKTARGKVRGRGASAAAESRKAKKPV				
		730	740	750	760	770
m988 . pep	640					
	PIKVKKRKGKSX					
a988		PIKVKKRKGKSX				
		790				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2985>:

g989 . seq	1	ATGACCCCTT TCACACTGAA AAAAACGTC CTGCTGCTCG GCACTGCCTT
	51	TGCCGCCGA TCTGTCCACG CATCCGGCTA CCACTTCGGC ACACAGTCGG
	101	TCAACGCGCA AAGCACGGCA AATGCCGCG ACGCCTCGAC CATCTTCTAC
	151	AATCCCAGCG GCCCTGACCAA ACTCGACAGC AGCCAGATT CCCTCAACGC
	201	CAACATCGTG CTGCCAGCA TTCATTATGA AGCAGATTCC GCCACCGACT
	251	TTACCGGGCT TCCCGTCAA GGTTCTAAAA AGCGCAAAAT CACCAAAACC
	301	ACGGTCGCAC CCCACATT TA CGCGCATAC AAAGTCAACG ACAATCTGAC
	351	CGTGGGCTTG GCGCTGTACG TCCCGCTGG CTCTGCCACC GAATACGAAA
	401	AAGATTCCGT GTTGCGCCAC AACATCAACA AACTCGGTCT GACCAGCATC
	451	GCCGTCGAAC CTGTCGCCGC GTGGAAACTC AACGAACGCC ATTCCCTCGG
	501	CGCAGGCATC ATCGCCCAAC ATAATCCGC CGAACTGCGC AAATATGCCG
	551	ACTGAGGAAT CCCAAAAAAA GCGCAATGC TGCAAGCAAC ACCTTCTAAT
	601	CCTACTGCCG CTGCTCAAAT CAAGGCCGAC GGACACGCCG ATGTCAGG
	651	CAGCGATTGG GCGCTCGGCT ACCAACTGGC GTGGATGTGG GACATCAACG
	701	ACCGCGCGCG CGTGGCGCTG AACTACCGTT CCAAAGTTTC ACACACGCTC
	751	AAAGGCGATG CGGAATGGGC GGCAGACGGC GCGGCGCGA AACAAACAGTG
	801	GAATGACAAT ATGCTCACAC CGCTCGGT A CACGGGAAT GAAAAAGCCA
	851	GTGTAAAAAT CGTAACGCCCT GAGTCTTGT CGTACACGG CAGTACACAA

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901 GTGTCCGACA AAGCCGACCT GTTCGGCGAC GTAACTTGGA CGCGCCACAG
951 CCGCTTCAAT AAGGCGGAAC TGTTTTTGA AAAAGAAAAA AATATTGCTA
1001 ATGGCAAAAA ATCCGACCAC ACCACCATCA CCCCCAACTG GCGCAACACC
1051 TACAAAGTCG GCTTGGCGG TTCTTATCAA ATCAGCGAAC CGCTGCAACT
1101 GCGCGTCGGC ATCGCTTTG ACAAACCGCC TGTCGCAAC GCCGACTacC
1151 GCATGAACAG CCTGCCCCGAC GGCAACCGCA TCTGTTCTC CGCCGGCATG
1201 AAATACCATCA TCGGCAAAAA CCACGTGTCG GATGCCGCT ACACCCACAT
1251 CCACATCAAC GACACCGAGT ACCGCACCGC GAAGGCAAGC GGCAACGATG
1301 TGGACAGCAA AGGTGCGTCT TGCGCACGTT TCAAAAACCA CGCCGACATC
1351 ATCGGCCTGC AATACACCTA CAAATTCAAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2986; ORF 989.ng>:

g989.pep

```

1 MTPFTLKKTV LLLGTAFAAA SVHASGYHFG TQSVNAQSTA NAADASTIFY
51 NPAGLTKLDS SQISVNANTV LPSIHYEADS ATDFTGLPVQ GSKNGKITKT
101 TVAPHIYGAY KVNDNLTVCL GVYVPFGSAT EYEKDSVLRH NINKLGLTSI
151 AVEPVAWKL NERHSFGAGI IAQHNSAELR KYAD*GIPKK AQMLQATPSN
201 PTAAQAQIKAD GHADVKGSDW GVGYQLAWMW DINDRARVGV NYRSKVSHTL
251 KGDAEWAADG AAAKQOWNDN MLTPLGYTAN EKASVKIVTP ESLSVHGMYK
301 VSDKADLFGD VTWTRHSRFN KAELFFEKEK NIANGKKSDR TTITPNWRNT
351 YKVGVLGGSYQ ISEPLQLRVG IAFDKPPVRN ADYRMNSLPD GNRIWFSAGM
401 KYHIGKNHVV DAAYTHIHN DTSYRTAKAS GNDVDSKGAS CARFKNHADI
451 IGLQYTYKFK *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2987>:

m989.seq

```

1 ATGACCCCCCT CCGCACTGAA AAAAACCGTC CTGCTGCTCG GCACTGCCTT
51 TGCCCGCGCA TCCGTCCACG CATCCGGCTA CCACTCGGC ACACAGTCGG
101 TCAACCGCGCA AAGCACCGCA AATGCCGCGG CGCGAGAAC CGCCGACGCA
151 TCGACCATCT TCTACAAACCC TGCCGGCTCG ACCAAACTCG ACAGCAGCCA
201 GATTCCCGTC AACGCCAACA TCGTGCTGCC CAGCATTCTAT TATGAGGGCGG
251 ATTCCCGCAAC CGACTTTACC GGGCTTCCCG TCCAAGGTTG GAAAAGCGGC
301 AAAATCACCA AAACCACCGT CGCGCCCCAC ATCTACGGCG CATACAAAGT
351 CAACGACAAT CTGACCGTGG GCTTGGCGT GTACGTCCCC TTCCGCTCTG
401 CCACCGAATA CGAAAAAGAT TCCGTGTGCG GCCACAAACAT CAACAAACTC
451 GGTCTGACCA GCATCGCCGT CGAACCTGTC GCGCGTGGAA AACTCAACGA
501 CCGCCATTCC TTCTGGCGAG GCATCATCGC CCAACATACT TCCCGCGAAC
551 TGCCTAAATA TGCCGACTGG GGGATTAAGA GTAAAGCAGA GATATTGACG
601 GCAAAACCGC CCAAACCTAA CGGTGTAGCC GAAGCTGCAA AAATTCAAGGC
651 CGACGGACAC CGCGATGTCA AAGGCAGCGA TTGGGGCTTC GGCTACCAAC
701 TGGCGTGGAT GTGGGACATC AACGACCGTG CGCGCGTGGG CGTGAACATAC
751 CGTTCCAAGG TCTCGCACG GCTCAAAGGC GATGCGGAAT GGGCGCGAGA
801 CGGCGCGGC GCGAAAGCAA TGTGGAGTAC GATGCTTGCA GCAAACGGCT
851 ACACCGCGAA TGAAAAAGCC CGCGTTAAAAA TCCTTACGCC TGAGTCTTTG
901 TCCGTACACG GTATGTACAA AGTGTCCGAT AAAGCCGACC TGTTCGGCGA
951 CGTAACCTGG ACACGCCACA GCGCCTTCGA TAAGGGGAA CTGGTTTTTG
1001 AAAAGAAAAA ACCCGTCGTC AAAGGCAAAT CCGACCGCAC CACCATCACC
1051 CCCAACTGGC GCAACACCTA CAAAGTCGGC TTCTGGCGTT CTTATCAAAT
1101 CAGCGAACCG CTGCACTGC CGCGCGGCAT CGCTTTGAC AAATCGCCCG
1151 TCCGCAACCGC CGACTACCGC ATGAAACAGCC TACCCGACGG CAACCGCATE
1201 TGGTTCTCG CCGGTATGAA ATACCATATC GTTAAAGAAC ACGTCGTGCA
1251 TGCCGCTAC ACCCACATCC ACATCAACGA CACAGCTAC CGCACGGCGA
1301 AGGCAAGCGG CAACGATGTG GACAGCAAAG CGCGCTCTC CGCACGTTTC
1351 AAAAACACG CCGACATCAT CGGTCTGCAA TACACCTACA AATTCAAATA
1401 A

```

This corresponds to the amino acid sequence <SEQ ID 2988; ORF 989>:

m989.pep

```

1 MTPSALKKTV LLLGTAFAAA SVHASGYHFG TQSVNAQSTA NAAAAEAADA
51 STIFYNPAGL TKLDSSQISV NANIVLPSIH YEADSATDFT GLPVQGSKSG
101 KITKTTVAPH IYGAYKVNDN LTVGLGVYVP FGSATEYEKD SVLRHNINKL
151 GLTSLAVEPV AAWKLNDRHS FGAGIIAQHT SAEILRKYADW GIKSKAEIL
201 AKPPPKNGVA EAAKIQFDGH ADVKGSDWGF GYQLAWMWDI NDRARVGVNY
251 RSKVSHTLKG DAEWAADGAA AKAMWSTMLA ANGTYANEKA RVKIVTPESL
301 SVHGMYKVSD KADLFGDVTW TRHSRFDKAE LVFEKEKTVV KGKSDRTTIT

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351 PNWRNTYKVG FGGSYQISEP LQLRAGIAFD KSPVRNADYR MNSLPDGNI  
 401 WFSAGMKYHI GKNHVVDAAY THIHINDTSY RTAKASGNDV DSKGASSARF  
 451 KNHADIIGLQ YTYKFK\*

Computer analysis of this amino acid sequence gave the following results:  
Homology with a predicted ORF from *N. gonorrhoeae*

**g989/m989** 90.0% identity in 468 aa overlap

<b>g989.pep</b>	10            20            30            40            50
	MTPFTLKKTVLLLGTAFAAAASVHASGYHFGTQSVNAQSTANAA-----DASTIFYNPAGL
<b>m989</b>	10            20            30            40            50            60
	MTPSALKTVLLLGTAFAAAASVHASGYHFGTQSVNAQSTANAAAADASTIFYNPAGL
<b>g989.pep</b>	60            70            80            90            100            110
	TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKNGKITKTTVAPHYGYAKVNDN
<b>m989</b>	70            80            90            100            110            120
	TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKSGKITKTTVAPHYGYAKVNDN
<b>g989.pep</b>	120            130            140            150            160            170
	LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAWKLNERHSFGAGIIAQHN
<b>m989</b>	130            140            150            160            170            180
	LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAWKLNDRHSFGAGIIAQH
<b>g989.pep</b>	180            190            200            210            220            230
	SAELRKYADXGIPKKAQMLQATPSNPTA---AAQIKADGHADVKGSDWGVGYQLAWMWDI
<b>m989</b>	190            200            210            220            230            240
	SAELRKYADWGIKSKEILTAKPPKPNVGAEAAKIQADGHADVKGSDWGFHYQLAWMWDI
<b>g989.pep</b>	240            250            260            270            280            290
	NDRARGVNVYRSKVSHTLKGDAEWAADGAAAKQQWNDNMLTPLGYTANEKASVKIVTPES
<b>m989</b>	250            260            270            280            290
	NDRARGVNVYRSKVSHTLKGDAEWAADGAAAKAMWS-TMLAANGYTANEKARVKIVTPES
<b>g989.pep</b>	300            310            320            330            340            350
	LSVHGMVKVSDKADLFGVTWTRHSRFNKAELFFEKEKNIANGKSDRTTITPNWRNTYK
<b>m989</b>	300            310            320            330            340            350
	LSVHGMVKVSDKADLFGVTWTRHSRFDKAELVFEKEKTVVKGK-SDRTTITPNWRNTYK
<b>g989.pep</b>	360            370            380            390            400            410
	VGLGGSYQISEPLQLRGIAFDKPPVRNADYRMNSLPDGNIWFSAGMKYHIGKNHVDA
<b>m989</b>	360            370            380            390            400            410
	VGFGGSYQISEPLQLRGIAFDKSPVRNADYRMNSLPDGNIWFSAGMKYHIGKNHVDA
<b>g989.pep</b>	420            430            440            450            460
	AYTHIHINDTSYRTAKASGNDVDSKGASCARFKNHADIIGLQTYTYKFKX
<b>m989</b>	420            430            440            450            460
	AYTHIHINDTSYRTAKASGNDVDSKGASSARFKNHADIIGLQTYTYKFKX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2989>:

**a989.seq**

1	ATGACCCCTT CCGCACTGAA AAAAACCGTC CTACTGCTCG GCACTGCCTT
51	TGCCGCCGCA TCCGCACAAG CCTCCGGCTA CCACTCGGC ACACAGTCGG
101	TCAACGGCA AAGCACGGCA AATGCCCGCG CGCGAGAACG CGCCGACGCA
151	TCGACCATCT TCTACAACCC TGCCGGCCTG ACCAAACTCG ACAGCAGCCA
201	GATTCCGTC AACGCCAACA CGTGCTGCC CAGCATTCTAT TATGAGGCC
251	ATTCCGCCAC CGCTTTTACCGGGCTTCCCG TCCAAGGTTC GAAAAGCGGC

301 AAAATCACCA AAACCACGGT CGCGCCCCAC ATCTACGGCG CATAACAAAGT  
 351 CAACGACAAT CTGACCGTAG GCTTGGCGT GTACGTCCCC TTGGTCTG  
 401 CCACCGAATA CGAAAAGAT TCCGTGTTGC GCCACAACAT CAACAAACTC  
 451 GGCTCTGACCA GCATCGCCGT CGAACCTGTC GCCGCGTGG AACTCAACGA  
 501 ACGCCATTCC TTGGCGCGAC GCATCATCGC CCAACATACT TCCGCGGAGC  
 551 TGCGCAAATA TGCGACTGG GGGATTATGG AAAAGCGAA AGCACTAAAA  
 601 GAAACACCCCC CCAATCAAC TAAAGCGCC CAAATCAAAG CCGACGGACA  
 651 CGCCGATGTC AAAGGCAGCG ATTGGGGCTT CGGCTACCAA CTGGCGTGG  
 701 TGTGGGACAT CAACGACCGT GCGCGCTGG GCGTGAACTA CGCTTCAA  
 751 GTCTCACACA CGCTCAAAGG CGATGCCGAA TGGGGCGAG ACCACGCAAT  
 801 GGCAGAACAG TTATGGGATG CAAACAAACT CGCACTGCTC GGCTACACGC  
 851 CAAGCGAAAA AGCCCGCGTT AAAATCGTTA CGCCCGAGTC TTGTCCTGTA  
 901 CACGGTATGT ACAAAAGTGTG CGACAAAGCC GACCTGTTCG GCGACGTAAC  
 951 TTGGACGCGC ACAGCGCGT TCGATAAGGC GGAACCTGGTT TTGAAAAG  
 1001 AAAAACCAT CGTCAACGGC AAATCCGAC GCACCAAC CACCCCCAAC  
 1051 TGGCGCAACA CCTACAAAGT CGGCTCGGC GGTTCTTATC AAATCAGCGA  
 1101 ACCGCTGCAA CTGCGCGCC GCATCGCTT TGACAAATCG CCCGTCGCA  
 1151 ACGCCGACTA CCGCATGAAC AGCCTGCCG ACGGCAACCG CATCTGGTTC  
 1201 TCCGCCGGCA TGAAATACCA TATCGCAAA AACACGTCG TCGATGCCGC  
 1251 CTACACCCAC ATCCACATCA ACGACACCG CTACCCACG GCGAAGGCAA  
 1301 GCGGCAACGA TGTGGACAGC AAAGGCAGCGT CTTCGGCACG TTCAAAAAC  
 1351 CACGCCGACA TCATCGGCCT GCAATACACC TACAAATTCA AATAA

This corresponds to the amino acid sequence <SEQ ID 2990; ORF 989.a>:

a989.pep

```

1  MTPSALKKTV LLLGTAFAAA SAQASGYHFG TQSVNAOSTA NAAAAEAADA
51 STIFYNPAGL TKLDSSQISV NANIVLPSIH YEADSATDFT GLPVQGSKSG
101 KITKTTVAPH IYGAYKVNDN LTVGLGVYVP FGSATEYEKD SVLRHNINKL
151 GLTSIAVEPV AAWKLNERHS FGAGIIAQHT SAEELRKYADW GIMEKAKALK
201 ETPPNPTKAA QIKADGHADV KGSDWGFYQ LAWMWDINDR ARVGVNYRSK
251 VSHTLKGDAE WAADDAMAKQ LWADKALL GYTPSEKARV KIVTPESLW
301 HGMYKVSDKA DLFGDVTWTR HSRFDKAELV FEKEKTIWNG KSDRTTITPN
351 WRNTYKVGF GSYQISEPLQ LRGIAFDKS PVRNADYRMN SLPDGNIW
401 SAGMKYHIGK NHVVDAAYTH IHINDTSYRT AKASQNDVDS KGASSARFKN
451 HADIIGLQYT YKFK*
  
```

m989/a989

93.1% identity in 467 aa overlap

m989.pep

	10	20	30	40	50	60
m989.pep	MTPSALKKTV	LLLGTAFAAA	SVHASGYHFG	TQSVNAOSTA	NAAAAEAADA	STIFYNPAGL
a989						

a989

	10	20	30	40	50	60
m989.pep	MTPSALKKTV	LLLGTAFAAA	SAQASGYHFG	TQSVNAOSTA	NAAAAEAADA	STIFYNPAGL
a989						

m989.pep

	70	80	90	100	110	120
m989.pep	TKLDSSQISV	NANIVLPSIH	YEADSATDFT	GLPVQGSKSG	KITKTTVAPH	IYGAYKVNDN
a989						

a989

	70	80	90	100	110	120
m989.pep	TKLDSSQISV	NANIVLPSIH	YEADSATDFT	GLPVQGSKSG	KITKTTVAPH	IYGAYKVNDN
a989						

m989.pep

	130	140	150	160	170	180
m989.pep	LTVGLGVYV	PFGSATEYEKDSV	LRHNINKLGLTSIAVEPVA	AWKLNDRHSFGAGIIAQHT		
a989						

a989

	130	140	150	160	170	180
m989.pep	LTVGLGVYV	PFGSATEYEKDSV	LRHNINKLGLTSIAVEPVA	AWKLNERHSFGAGIIAQHT		
a989						

m989.pep

	190	200	210	220	230	240
m989.pep	SAELRKYADWG	IKSKAELITA	KPPKPN	VAEAAKIQADGHAD	VKGSDWGFYQ	LAWMWDI
a989						

a989

	190	200	210	220	230	240
m989.pep	SAELRKYADWG	IKSKAELITA	KPPKPN	VAEAAKIQADGHAD	VKGSDWGFYQ	LAWMWDI
a989						

m989.pep

	250	260	270	280	290	299
m989.pep	NDRARGV	YRSKV	SHTLKGDAE	WAADGAAKAMW	-STMLAANGY	TANEKARV
a989						

a989

	250	260	270	280	290	299
m989.pep	NDRARGV	YRSKV	SHTLKGDAE	WAADGAAKAMW	-STMLAANGY	TANEKARV
a989						

1407

	240	250	260	270	280	290	
m989 . pep	300	310	320	330	340	350	359
	LSVHGMYKVSDKADLFGDVTWTRHSRFDKAELVFEKEKTVVKGKSERTTITPNWRNTYKV						
a989	300	310	320	330	340	350	
	LSVHGMYKVSDKADLFGDVTWTRHSRFDKAELVFEKEKTVVKGKSERTTITPNWRNTYKV						
m989 . pep	360	370	380	390	400	410	419
	GFGGSYQISEPLQLRAGIAFDKSPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVVDA						
a989	360	370	380	390	400	410	
	GFGGSYQISEPLQLRAGIAFDKSPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVVDA						
m989 . pep	420	430	440	450	460		
	YTHIHINDTSYRTAKASGNDVDSKGASSARFKNHADIIGLQYTYKFKX						
a989	420	430	440	450	460		
	YTHIHINDTSYRTAKASGNDVDSKGASSARFKNHADIIGLQYTYKFKX						

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2991>:

m990 . seq	1	ATGTTCAAGAG CTCAGCTTGG TTCAAATACT CGTTCTACCA AAATCGGCGA
	51	CGATGCCGAT TTTTCATTTT CAGACAAGCC GAAACCCGGC ACTTCCATT
	101	ATTTTCCAG CGGTAAAACC GATCAAATT CATCGAATA TGCGTATGAC
	151	GAAATCAATA TCCAAGGTAA AAATTACAAT AGCGGCATCC TCGCCGTGCA
	201	TAATATGCCG GTTGTCAAA AATATATTAC AGAGAAGTAT GGGGCTGATT
	251	TAAAGCAGGC GGTAAAAGT CAATTACAGG ATTATACAA ACAAGACCG
	301	GAAGCTTGGG CAGAAAATAA AAAACGGACT GAGGAGGCCT ATATAGCACA
	351	GTTTGAACA AAATTTAGTA CGCTAACAA GACGATGCC GATTTAATT
	401	ATAAATTGGT AGAAGATTCC GTACTCACTC CTCATAGTAA TACATCACAG
	451	ACTAGTCTCA ACAACATCTT CAATAAAAAA TTACACGTCA AAATCGAAAA
	501	CAAATCCCAC GTGCCGGAC AGGTGTTGGA ACTGACCAAG ATGACGCTGA
	551	AAAGATTCCCT TTGGGAACCG CGCCGCCATT CGCACATCCA TACGCTGGAA
	601	ACTTCCGATA ATGCCGCAT CGCCCTGAAC ACGAAAGATG AAAAACTGAC
	651	CGTCCATAAG GATTATGCCG GCGGCGCGGA TTTCTGTTG GCCTACGACG
	701	TGCGGGAGTC GGACGAACCC GCCCTGACCT TTGAAGACAA ACTCAGCGGA
	751	CAATCCGGCG TGGTTTGGGAC CGCCGCCG GAAAATCTGA AAACGCTCGA
	801	CGGGCGAAA CTGATTGCCG CAAAAACGGC GGATTCGGT TCGTTTGCCT
	851	TTAACACAAA TTACCGCGAG GGACTGTAGC ATTATTGCT CAAAGCAATGC
	901	GAAGGGGGAT TTTGTTTGGG CGTGCAGCGT TTGGCTATCC CCGAGGGCGGA
	951	AGCGGTTTA TATGCCAAC AGGCTTATGC GGCAAATACT TTGTTTGGG
	1001	TGCGTCCCGC CGACAGGGC GACGACGTGT ATGCCGCCGA TCCGCTCCGT
	1051	CAAAATTGT GGCTCGCTT CATCGCCGGC CGGTGCGCATC AAAATATACG
	1101	GGGCGGCG GCTCGGGACG GGTGGCGCAA AGGCGTGCAG ATCGGCGCG
	1151	AGGTGTTGT ACGGCAAAT GAAGGCAGCC GACTGGCAAT CGCGTGTATG
	1201	GGCGGCAGGG CGGGCAGCGA CGCATCGTC AACGGCAAAG GCGGTGCGGC
	1251	AGGCAGTGTATGGTATGGTATGGTATGGTATGGTATGGTATGGTATGGTATGGT
	1301	AGTTGCGCGA TAAACAAACG GGTGCGTATT TGGACGGCTG GTTGCATAC
	1351	CAACGTTCA AACACCGCAT CAATGATGAA AACCGTGCAG AACGCTACAA
	1401	AACCAAAGGT TGGACGGCTT CTGTCGAAGG CGGCTACAAC GCGCTTGTGG
	1451	CGGAAGGCAT TGTCGAAAGG GGCAATAATG TGCGGTTTA CCTACAACCG
	1501	CAGGCGCAGT TTACCTACTG GGGCGTAAAC GGGCGCTTTA CGCACAGCGA
	1551	GGGGACGGCG GTCCGACTGC TCAGGCGCGG TCAGTGGCAA AGCCCGCGCG
	1601	GCATTGGGC AAAAACCGT TTTGCTTGC GTAACGGTGT CAATCTTCAG
	1651	CCTTTGCGC CTTTAATGTT TTTGACAGG TCAAAATCTT TCGCGTGGGA
	1701	AATGGACGGC GAAAAACAGA CGCTGGCAGG CAGGACGGCA CTCGAAGGGC
	1751	GGTTCGGTAT TGAAGCCGGT TGGAAAGGCC ATATGTCCGC ACGCATCGGA
	1801	TATGGCAAAA GGACGGACGG CGACAAAGAA GCGCATTGT CGCTCAAATG
	1851	GCTGTTTGAA

This corresponds to the amino acid sequence <SEQ ID 2992; ORF 990>:

m990 . pep

```

1  MFRAQLGSNT RSTKIGDDAD FSFSDKPKPG TSHYFSSGKT DQNSSEYGYD
51  EINIQGKYN SGINLAVDNMP VVKKYITEKY GADLKQAVKS QLQDLYKTRP
101  EAWEENKKRT EEAYIAQFGT KFSTLKQTMP DLINKLVEDS VLTPHSNTSQ
151  TSLNNIFNKK LHVKIENKSH VAGQVLELT KMTLKDSLWEP RRHSDIHTLE
201  TSDNARIRLN TKDEKLTVHK DYAGGADFLF GYDVRESDEP ALTFEDKVSG
251  QSGVVLERP ENLKTLGDK LIAAKTADSG SFAFKQNYRQ GLYELLLKQC
301  EGGFCLGVQR LAIPEAEAVL YAQQAYAANT LFGLRAADRG DDVYAADPSR
351  QKLWLRFIGG RSHQNIRGGA AADGWRKGQVQ IGGEVFVRQN EGSRILAIGVM
401  GGRAGQHASV NGKGGAAAGSD LYGYGGVY AWHQLRDKQT GAYLDGWLQY
451  ORFKHRINDE NRAERYKTKG WTASVEGGYN ALVAEGIVGK GNVRFYLQP
501  QAQFTYLGVN GGFTDSEGT A VGLLGSQWQ SRAGIRAKTR FALRNGVNLQ
551  PFAAFNVLHR SKSFGVEMDG EKQTLAGRTA LCCRGIEAG WKGHMSARIG
601  YGKRTDGDKE AALS LKWL*F

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2993>:

```

a990.seq
1  ATGTTCAAGAG CTCAGCTTGG TTCAAAATACT CGTTCTACCA AAATCGGCCA
51  CGATGCCGAT TTTTCATTT CAGACAAGCC GAAACCCGGC ACTTCCCAT
101  ATTTTTCCAG CGGTAAACCC GATCAAAATT CATCCGAAATA TGGGTATGAC
151  GAAATCAATA TCCAAGGTA AAACATACAAT AGCAGCATAAC TCGCCGTCGA
201  TAATATGCC C GTTGTAAAGA AATATATTAC AGATACTTAC GGGGATAATT
251  TAAAGGATGC GGTAAAGAAG CAATTACAGG ATTATATACAA ACAAGACCC
301  GAAGCTTGGG AAGAAAATAA AAAACGGACT GAGGAGGCCT ATATAGAAC
351  GCTTGGACCA AAATTTAGTA TACTCAAACA GAAAAACCCC GATTTAATT
401  ATAATATTGGT AGAAGATTCC GTACTCTACT CTCATAGTAA TACATCACAG
451  ACTAGTCTCA AACAACATCTT CAATAAAAAA TTACACGTCA AAATCGAAAA
501  CAAATCCCAC GTCGCCGAG AGGTGTTGGA ACTGACCAAG ATGACGCTGA
551  AAGATTCCCT TTGGGAACCG CGCCGCCATT CGCAGATCCA TATGCTGGAA
601  ACTTCCGATA ATGCCCGCAT CGCCCTGAAC ACGAAAGATG AAAAACTGAC
651  CGTCCATAAA GCGTATCAGG GCGGTGCGGA TTTCTGTTC GGCTACGACG
701  TCGGGAGTC GGACAAACCC GCCCTGACCT TTGAAGAAAA AGTCAGCGGA
751  CAATCCGGCG TGGTTTTGGA ACGCCGGCCG GAAAATCTGA AAACGCTCGA
801  CGGGCGCAA CTGATTGCGG CGGAAAAGGC AGACTCTAAT TCGTTTGCCTG
851  TTAAACAAAAA TTACCGGAG GGACTGTACG AATTATTGCT CAAGCAATGC
901  GAAGGCGGAT TTTGCTTGGG CGTGCAGCGT TTGGCTATCC CCGAGGCGGA
951  AGCGGTTTTA TATGCCAAC AGGCTTATGC GGCAAAACT TTGTTCGGGC
1001  TGCCTGCCGC CGACAGGGC GACGACGTGT ATGCCGCCGA TCCGTCCTCGT
1051  CAAAAATTGT GGCTGCGCTT CATCGCCGGC CGGTGCGCATC AAAATATACG
1101  GGGCGGCCG GCTCGGGACG GCGGGCGCAA AGGCGTGCAC ATCGGCGGCCG
1151  AGGTGTTTGT ACAGGCAAAAT GAAGGCAGCC GGCTGGCAAT CGGCGTGTATG
1201  GCGGGCAGGG CTGGCCAGCA CGCATCAGTC AACGGCAAAG GCGGTGCGGC
1251  AGGCAGTTAT TTGCATGGTT ATGGCGGGGG TGTATTGCT GCGTGGCATC
1301  AGTTGCGCGA TAAACAAACG GGTGCGTATT TGGACGGCTG GTTGAATAC
1351  CAACGTTTCA AACACCGCAT CAATGATGAA AACCGTGC GG AACGCTACAA
1401  AACCAAAGGT TGGACGGCTT CTGTCGAAGG CGGCTACAAC GCGCTTGTGG
1451  CGGAAGGCCT GTGCGGAAA GGCAATAATG TGGCGTTTTA CCTGCAACCG
1501  CAGGCAGCT TTACCTACTT GGGCGTAAAC GCGGGCTTTA CCGACAGCGA
1551  GGGGACGGCG GTCGGACTGC TCAGGCGAGG TCACTGGCAA AGCCGCGCCG
1601  GCATTGGC AAAACCCGT TTTGCTTGC GTAACGGTGT CAATCTTCAG
1651  CCTTTGCGC CTTTTAATGT TTTGACAGG TCAAAATCTT TCGGCGTGG
1701  AATGGACGGC GAAAAACAGA CGCTGGCAGG CAGGACGGCG CTCGAAGGGC
1751  GGTTCGGCAT TGAAGCCGGT TGGAAAGGCC ATATGTCCGC ACGCATCGGA
1801  TACGGCAAAA GGACGGACGG CGACAAAGAA GCGCATTGT CGCTCAAATG
1851  GCTGTTTGAA

```

This corresponds to the amino acid sequence <SEQ ID 2994; ORF 990.a>:

```

a990.pep
1  MFRAQLGSNT RSTKIGDDAD FSFSDKPKPG TSHYFSSGKT DQNSSEYGYD
51  EINIQGKYN SGINLAVDNMP VVKKYITDTY GDNLKDAVKK QLQDLYKTRP
101  EAWEENKKRT EEAYIEQLGP KF~LKQKNP DLINKLVEDS VLTPHSNTSQ
151  TSLNNIFNKK LHVKIENKSH VAGQVLELT KMTLKDSLWEP RRHSDIHTLE
201  TSDNARIRLN TKDEKLTVHK AYQGGADFLF GYDVRESDKP ALTFEEKVSG
251  QSGVVLERP ENLKTLGDK LIAAEKADSN SFAFKQNYRQ GLYELLLKQC
301  EGGFCLGVQR LAIPEAEAVL YAQQAYAANT LFGLRAADRG DDVYAADPSR
351  QKLWLRFIGG RSHQNIRGGA AADGRRKGQVQ IGGEVFVRQN EGSRILAIGVM

```

401 GGRAGQHASV NGKGGAAQSY LHGYGGGVYA AWHQLRDQQT GAYLDGWLQY  
 451 QRFKHRINDE NRAERYTKKG WTASVEGGYN ALVAEGVVGK GNNVRFYLQP  
 501 QAQFTYLGVN GGFTDSEGTA VGLLGSGQWQ SRAGIRAKTR FALRNGVNLO  
 551 PFAAFNVLHR SKSFGVEMDG EKQTLAGRTA LEGRFGIEAG WKGHMSARIG  
 601 YGKRTDGDKE AALSLKWLF

m990/a990 96.0% identity in 619 aa overlap

	10	20	30	40	50	60
m990.pep	MFRAQLGSNTRSTKIGDDADFSFSKPKPGTSHYFSSGKTDQNSSEYGYDEINIQGKNYN					
a990	MFRAQLGSNTRSTKIGDDADFSFSKPKPGTSHYFSSGKTDQNSSEYGYDEINIQGKNYN	10	20	30	40	50
						60
m990.pep	SGILAVDNMPVVKKYITEKYGADLKQAVKSQLODLYKTRPEAWAENKKRTEEAYIAQFGT	70	80	90	100	110
a990	SGILAVDNMPVVKKYITDTYGDNLKDAVKKQLQDLYKTRPEAWEENKKRTEEAYIEQLGP	70	80	90	100	110
						120
m990.pep	KFSTLKVQMPDLINKLVEDSVLTPHSNTSQTSLNNI FNKKLHVKIEENKSHVAGQVLELTK	130	140	150	160	170
a990	KFSILKQKQNPDPDLINKLVEDSVLTPHSNTSQTSLNNI FNKKLHVKIEENKSHVAGQVLELTK	130	140	150	160	170
						180
m990.pep	MTLKDSLWEPRRHSDIHLTSDNARIRLNKDEKLTVHKDYAGGADFLFGYDVRESDEP	190	200	210	220	230
a990	MTLKDSLWEPRRHSDIHMLETSDNARIRLNKDEKLTVHKAYQGGADFLFGYDVRESDKP	190	200	210	220	230
						240
m990.pep	ALTFEDKVSGQGVVLERPENLKTLDGRKLIAAKTADSGSFIAFKQNYRQGLYELLKQC	250	260	270	280	290
a990	ALTFEEKKVSGQGVVLERPENLKTLDGRKLIAAEKADSNSFAFKQNYROGLYELLKQC	250	260	270	280	290
						300
m990.pep	EGGFCLGVQRLAIPAEAVLYAQQAYAANTLFGLRAADRGDDVYADPSRQKLWLRFIGG	310	320	330	340	350
a990	EGGFCLGVQRLAIPAEAVLYAQQAYAANTLFGLRAADRGDDVYADPSRQKLWLRFIGG	310	320	330	340	350
						360
m990.pep	RSHQNIRGGAAADGWRKGVQIGGEV FVRQNEGSRLAIGVMGRAGQHASVNGKGGAAAGSD	370	380	390	400	410
a990	RSHQNIRGGAAADGRRKGVQIGGEV FVRQNEGSRLAIGVMGRAGQHASVNGKGGAAAGSY	370	380	390	400	410
						420
m990.pep	LYGYGGGVYAAWHQLRDQQTGAYLDGWLQYQRFKHRINDENRAERYKTKGWTASVEGGYN	430	440	450	460	470
a990	LHGYGGGVYAAWHQLRDQQTGAYLDGWLQYQRFKHRINDENRAERYKTKGWTASVEGGYN	430	440	450	460	470
						480
m990.pep	ALVAEGIVGKGNVRFYLQPQAQFTYLGVNNGFTDSEGTAVGLLGSGQWQSRAKTR	490	500	510	520	530
a990	ALVAEGVVGKGNVRFYLQPQAQFTYLGVNNGFTDSEGTAVGLLGSGQWQSRAKTR	490	500	510	520	530
						540
m990.pep	FALRNGVNLOPFAAFNVLHRSKSFVEMDG EKQTLAGRTALEGRFGIEAGWKGHMSARIG	550	560	570	580	590
a990	FALRNGVNLOPFAAFNVLHRSKSFVEMDG EKQTLAGRTALEGRFGIEAGWKGHMSARIG	550	560	570	580	590
						600

1410

	550	560	570	580	590	600
	610	620				
m990.pep	YGKRTDGDKEAALSLKWLFX					
a990	YGKRTDGDKEAALSLKWLFX					
	610	620				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2995>:

**g992.seq**

1	ATGTTCAAGAC GGCATCGGCA TTTGAAAAAT ATGCAGATTA AAAAATCAT
51	GAAATGGCTT CCCGTCGCCC TGTCGCTTT GGGCGCGTTG GGTTATACGG
101	GATATGACAG TGAGGCCTG CGGACGGCGG TTGCGTACT CGACGTTACTC
151	GGCACTGCAG GGGACGTGGG TTTCGACGCC CCCGTTCGCC GACGGGCATC
201	GGCAGAAATCC GGCCACAGCT ACACAGGCAC GGTGTCACAA GTCTATGACG
251	GCGATACCTT TCACGTCATC GACGGCAGAC GCGCGAAACA TAAAATTCGG
301	ATGGCGTATA TCGACGCACC GGAGATGAAA CAGGCTTACG GTACACGTT
351	GGCGGACAAAC CTGCGCGCC CGGGCGAGGG TAGGAAAGTC GTGACGTT
401	TGTTTGAAC CGACCGCTAT CAGCGCGAAG TGGCGCAGGT ATCCGCCGGC
451	AAAACCGATT TGACCGCTAT GCAAGGTGCAAG GACGGGGCGG CGTGCCTT
501	TAAAAGTTAT GCTAAAGAAC AGCAGGATAA GCGGGATTTC GCGACTATG
551	CCGACGCTCA AATTCAAGGGC GAAAGGGAAAC GCAAAGGATT GTGAAAGCT
601	AAAAATCCGC AAGCGCCGTG GGCCTACCGC CGGGCAGGCA GGAGCGGGCG
651	GGGCAATAAG GATTGGATGG ATTCCGTGGG CGAATGGTTG GGCATTGGT
701	AA

This corresponds to the amino acid sequence <SEQ ID 2996 ORF 992.ng>:

**g992.pep**

1	MFRRHRHLKN MQIKKIMKWL PVALSLIGAL GYTGYDSEAV RTAVAVLDVL
51	GTAGDVGFD A PVERRASAKS GHSYTGTVSK VYDGDTLHVI DGDGAKHHKIR
101	MAYIDAPEMK QAYGTRSRDN LRAAAEGRKV SVRVFETDRY QREVAQVSAG
151	KTDLNLMQVQ DGAAWHYKSY AKEQQDKADF ADYADAQIQA ERERKGLWKA
201	KNPQAPWAYR RAGRSGGGNK DWMDSVGEWL GIW*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2997>:

**m992.seq**

1	ATGTTCAAGAC GGCATCGGCA TTTGAAAAAT ATGCAGATTA AAAAATCAT
51	GAAATGGCTT CCCGTCGCCC TGTCGCTTT GGGCGCGTTG GGTTATACGG
101	GGTACGGCAG CGAGGCCGTG CGGACGGCGG TTGCGTACT CGACGTTACTC
151	GGCGGGCAG GGGACGCGGG TTCCGACGCC CCCGCCCCCC GCCGAGCATC
201	GGCAGAAATCC GGCCACCGCT ACACAGGCAC GGTGTCACAA GTCTATGACG
251	GCGACACCTT TCACGTTATC GACGGCAGC GCGCGAAACA CAAAATCCGG
301	ATGGCGTATA TCGACGCCGGC GGAGATGAAA CAGGCTTACG GCACGGCTT
351	GGCGGACAAAC CTGCGCGCC CGGGCGAAGG CAGGAAAGTC AGCGTSCGCG
401	TGTTGATAC CGACCGCTAC CAGCGCGAAG TGGCGCAGGT TTCTGTCGGC
451	AAAACCGATT TGACCGCTAT GCAAGGTGCAAG GACGGGGCGG CGTGCCTT
501	TAAAAGTTAT GCTAAAGAAC AGCAGGATAA GCGGGATTTC GCGGATTATG
551	CCGACGCTCA AATTCAAGGGC GAAAGGGAAAC GCAAAGGATT GTGAAAGCT
601	AAAAATCCGC AAGCGCCGTG GGCCTACCGC CGAGCAGGCA GGAGCGGGCG
651	GGGCAATAAG GATTGGATGG ATGCCGTGGG CGAATGGTTG GGCATTGGT
701	AA

This corresponds to the amino acid sequence <SEQ ID 2998; ORF 992>:

**m992.pep**

1	MFRRHRHLKN MQIKKIMKWL PVALSLIGAL GYTGYGSEAV RTAVAVLDVL
51	GAAGDAGSSDA PARRASAKS GHRYTGTVSK VYDGDTLHVI DGDGAKHHKIR
101	MAYIDAPEMK QAYGTRSRDN LRAAAEGRKV SVRVFETDRY QREVAQVSVG
151	KTDLNLMQVQ DGAAWHYKSY AKEQQDKADF ADYADAQIQA ERERKGLWKA
201	KNPQAPWAYR RAGRSGGGNK DWMDAVGEWL GIW*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 992 shows 96.1% identity over a 233 aa overlap with a predicted ORF (ORF 992) from *N. gonorrhoeae*

**m992/g992** 96.1% identity in 233 aa overlap

	10	20	30	40	50	60
m992.pep	MFRRHRHLKNMQIKKIMKWLPVALSLLGALGYTGYGSEAVRTAVAVLDVLGAAGDAGSDA					
g992						
	10	20	30	40	50	60
m992.pep	MFRRHRHLKNMQIKKIMKWLPVALSLLGALGYTGYDSEAVRTAVAVLDVLGCTAGDVGFD					
g992						
	70	80	90	100	110	120
m992.pep	PARRASAKSGHRYTGTISKVYDGDTLHVIDGDGAKHKIRMAYIDAPEMKQAYGTRSRDN					
g992						
	70	80	90	100	110	120
m992.pep	PVRRASAKSGHYSYGTISKVYDGDTLHVIDGDGAKHKIRMAYIDAPEMKQAYGTRSRDN					
g992						
	130	140	150	160	170	180
m992.pep	LRAAAEGRKVSVRVFETDRYQREVAQSVGKTDLNLMQVQDGAAWHYKSYAKEQQDKADF					
g992						
	130	140	150	160	170	180
m992.pep	LRAAAEGRKVSVRVFETDRYQREVAQVSAGKTDLNLMQVQDGAAWHYKSYAKEQQDKADF					
g992						
	190	200	210	220	230	
m992.pep	ADYADAQIQAERERKGLWKAKNPQAPWAYRRAGRSGGGNKDWMDAVGEWLGIX					
g992						
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2999>:

**a992.seq**

1	ATGTTCAGAC	GGCATCGGCA	TTTGAAAAT	ATGCAGATTAA	AAAAAAATCAT
51	GAATGGCTT	CCCGTCGCGCT	TGTCGCTTT	GGGTGCGTTG	GGTTATACGG
101	GTTACGGCAG	CGAGGCCTG	CGGACGGCGG	TTGCCGTACT	CGACGTACTC
151	GGCGCGGAG	GGGACGCGGG	TTCCGACCGG	CCCGCCCGCC	GGCGAGCATC
201	GGCGAAATCC	GGCCACCGCT	ACACAGGACG	GGTGTCCAAA	GCTATGACG
251	GGCGACACCTC	TCACGTTATC	GACGGCGACG	GCGCGAAACA	CAAATCCGG
301	ATGGCGTATA	TCGACGCGCC	GGAGATGAAA	CAGGCTTACG	GCACCGCTTC
351	GGCGGACAAAC	CTGCGCGGG	CGGGCGGAAGG	CAGGAAAGTC	AGCGTCCCGC
401	TGTTCGACAC	CGACCGCTAC	CAGTCGGAAT	TGGTCTAGGT	TTCTGTCCGC
451	AAAACCGATT	TGAACCTGTAT	GCAGGTGCGAC	GACGGGGCGG	CGTGGCATTAA
501	TAAAAGTTAT	GCTAAAGAAC	AGCAGGATAAA	GGCGGATTTT	GCGATTATAG
551	CCGACGCTCA	AATTCAAGGGC	GAAAGGGAAAC	GCAAAGGATT	GTGAAAGCT
601	AAAATCCGC	AAGGCCCGTG	GGCGTACCGC	CGGGCAGGCA	GGAGCGGCGG
651	GGGCAATAAG	GATTGGATGG	ATGCCGTGGG	CGAATGGTTG	GGCATTTGGT
701	AA				

This corresponds to the amino acid sequence <SEQ ID 3000; ORF 992.a>:

**a992.pep**

1	MFRRHRHLKN	MQIKKIMKWL	PVALSLLGAL	GYTGYGSEAV	RTAVAVLDVL
51	GAAGDAGSDA	PARRASAKS	GHRYTGTISKV	VYDGDTLHVI	DGDGAKHKIR
101	MAYIDAPEMK	QAYGTRSRDN	LRAAAEGRKV	SVRVFETDRY	QREVAQVSVG
151	KTDLNLQMVO	DGAAWHYKSY	AKEQQDKADF	ADYADAQIQA	ERERKGLWKA
201	KNPQAPWAYR	RAGRSGGGNK	DWMDAVGEWL	GIW*	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 992 shows 100.0% identity over a 233 aa overlap with a predicted ORF (ORF 992) from *N. meningitidis*

**a992/m992** 100.0% identity in 233 aa overlap

	10	20	30	40	50	60
a992.pep	MFRRHRHLKNMQIKKIMKWLVALSLLGALGYTGYGSEAVRTAVAVLDVLGAAGDAGSDA					
m992						
	10	20	30	40	50	60
a992.pep	PARRASAKSGHRYTGTISKVYDGDTLHVIDGDGAKHKIRMAYIDAPEMKQAYGTRSRDN					
m992						
	70	80	90	100	110	120
a992.pep	PARRASAKSGHRYTGTISKVYDGDTLHVIDGDGAKHKIRMAYIDAPEMKQAYGTRSRDN					
m992						
	70	80	90	100	110	120
	130	140	150	160	170	180

1412

a992.pep	LRAAAEGRKVSVRVFDTDRYQREVAQSVGKTDLNLMQVQDGAAWHYKSYAKEQQDKADF				
m992	LRAAAEGRKVSVRVFDTDRYQREVAQSVGKTDLNLMQVQDGAAWHYKSYAKEQQDKADF				
	130	140	150	160	170
	190	200	210	220	230
a992.pep	ADYADAQIQAERERKGLWAKNPQAPWAYRRAGRSGGGNKKDWMDAVGEWLGIWX				
m992	ADYADAQIQAERERKGLWAKNPQAPWAYRRAGRSGGGNKKDWMDAVGEWLGIWX				
	190	200	210	220	230

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3001>:

**g993.seq**

1	CTGAAAGTCG	TATTGGGCAG	TTTTCAAGGC	CCTTTGGATC	TGCTGCTCTA
51	CCTTATCCG	AAACAGAAACA	TCGATGTTCT	CGATATTCCG	ATGGTGAAAG
101	TTACCGGGCA	GTATCTGCAC	TATATTGCC	AAATGGAAAGC	CTATCAGTTT
151	GATTGGCGG	CGGAATATCT	TTTGATGGCG	GCAATGCTGA	TTGAAATCAA
201	ATCGCGCTG	CTGCTGCCG	GTACCGAACG	CGTCGAAGAC	GAAGAGGCCG
251	ACCCGGCTGC	CGAGTTGGTG	CGCCGTCCTC	TTGCCTACCGA	GCAAATGAAA
301	CTGGCGGCCG	AGGGTTTGGA	CGCGCTGCCG	CGTGCAGGAC	GGGATTTCGC
351	GTGGGCTTAC	CTGCCGCTGG	AAATTGCAAC	CGAGACGAAG	CTGCCCGAGG
401	TTTACATCGC	CGATTGATG	CAGGCATGGT	TGGGCATTCT	TTCTCGGGCA
451	AAACATACGC	GCAGCCACGA	AGTAATCCAA	GAAACCCCTT	CCGTGCGCGC
501	GCAAATGACG	GAATCCTGC	GCCGTTTGAA	CGAACACCGG	ATATGCAAGT
551	TTCACGCGCT	GTTCAATCCC	GAACAGGGCG	CGGCTTACGT	GATCGTCAAC
601	TTCATCGCCC	TGTTGGAGCT	TGCCAAAGAA	GGATTGGTCG	GAATCGTACA
651	GGAAGACGGT	TTCGGAGAAA	TCCGAATCAG	CCTCAATCAT	GAGGGGGCGC
701	ATTCAAGACGG	CATTTCCGC	ACACGGGGCG	GGCGCGATGT	CTTCTAA

This corresponds to the amino acid sequence <SEQ ID 3002 ORF 993.ng>:

**g993.pep**

1	LKVVLGSFQG	PLDLLLLYLIR	KQNIIDVLDIP	MVEITGQYLH	YIAQMEAYQF
51	<u>DIAAEYLLMA</u>	AMLIEIKSRL	LLPRTEAVED	EEADPRAELV	RRLLAYEQMK
101	LAAQGLDALP	RAGRDFAWAY	LPLEIAAEAK	LPEVYIADLM	QAWLGILSRA
151	KHTRSHHEVIQ	ETLSVRAQMT	AIRRLRNHEG	ICRFHALFNP	EQGAAYVIVN
201	<u>FIALEELAKE</u>	<u>GLVGIVQEDG</u>	<u>FGEIRISLNH</u>	<u>EGAHSDGIFG</u>	<u>TRGRDVF*</u>

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3003>:

**m993.seq**

1	TTGAAAGTCG	TATTGGGCAG	CTTCCAAGGC	CCTTTGGATC	TACTGCTGTA
51	TCTGATCCG	AAACAGAAATA	TCGACGTA	GGATATTCCG	ATGGTGAAAGA
101	TTACCGAGCA	GTATCTGCAC	TACATGCC	AAATGAAAC	CTATCAGTTT
151	GATTGGCGG	CGGAATATCT	TTTGATGCCA	GCAATGCTGA	TTGAAATCAA
201	ATCGCGCTG	CTGCTGCCG	GTACCGAACG	CGTCGAAGAC	GAAGAAGGCCG
251	ACCCGGCTGC	CGAGTTGGTG	CGCCGCTCTC	TGGCTTACCGA	ACAGATGAAAG
301	CTGGCGGCCG	AGGGTTTGGA	CGCGCTGCCG	CGAGCCGGAC	GGGATTTCGC
351	GTGGGCTTAC	CTGCCGCTGG	AAATTGCCG	CGAACCCAAG	CTGCCCGAAG
401	TCTATATTAC	CGACTTGACG	CAAGCGTGGC	TGGGTATTCT	GTCTCGGGCA
451	AAACACACGC	GCAGCCACGA	AGTAATCAA	GAAACCACAT	CCGTGCGCGC
501	GCAAATGACG	GAATCCTGC	GCCGTTTGAA	CGGACACCGA	ATATGCAAGT
551	TTCACGACCT	GTTCAATCCC	AAACAGGGCG	CGGCTTACGT	GTCGTCAC
601	TTCATCGCAC	TGTTGGAGCT	TGCCAAAGAA	GGATTGGTCG	GAATCGTACA
651	GGAAGACGGT	TTCGGAGAAA	TCCGAATCAG	CCTCAATCAT	GAGGGGGCGC
701	ATTCAAGACGG	CATTTCCGC	ACACGAGGGC	GGCGCGATGT	GTTCCTAA

This corresponds to the amino acid sequence <SEQ ID 3004; ORF 993>:

**m993.pep**

1	LKVVLGSFQG	PLDLLLLYLIR	KQNIIDVLDIP	MVKITEQYLH	YIAQIETYQF
51	<u>DIAAEYLLMA</u>	AMLIEIKSRL	LLPRTEVED	EEADPRAELV	RRLLAYEQMK
101	LAAQGLDALP	RAGRDFAWAY	LPLEIAVEAK	LPEVYITDLT	QAWLGILSRA
151	KHTRSHHEVIK	ETLSVRAQMT	AIRRLRNHG	ICRFHDLFNP	KQGAAYVIVN
201	<u>FIALEELAKE</u>	<u>GLVRIVQEDG</u>	<u>FGEIRISLNH</u>	<u>EGAHSDGIFG</u>	<u>TRGRDVF*</u>

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 993 shows 93.1% identity over a 248 aa overlap with a predicted ORF (ORF 993) from *N. gonorrhoeae*

**m993/g993** 93.1% identity in 248 aa overlap

<b>m993.pep</b>	10            20            30            40            50            60 LKVVLSFQGPLDLLLLLIRKQNI DVL DIPMV KITEQYLHYIAQIETYQFDLAAEYLMA      :     :     :     :     :     :     :     :     :     :     :
<b>g993</b>	LKVVLGSFQGPLDLLLLLIRKQNI DVL DIPMV KITEQYLHYIAQMEAYQFDLAAEYLMA 10            20            30            40            50            60
<b>m993.pep</b>	70            80            90            100            110            120 AMLIEIKSRLLLPRTEVDEEADPRAELVRRLLAYEQMKLAAQGLDALPRAGRDFAWAY      :     :     :     :     :     :     :     :     :     :     :     :
<b>g993</b>	AMLIEIKSRLLLPRTEA VDEEADPRAELVRRLLAYEQMKLAAQGLDALPRAGRDFAWAY 70            80            90            100            110            120
<b>m993.pep</b>	130            140            150            160            170            180 LPLEIAVEAKLPEVYITDLTQAWLGILSRAKHTRSHEVIKETISVRAQM TAILRRLNNGH      :     :     :     :     :     :     :     :     :     :     :     :
<b>g993</b>	LPLEIAEAKLPEVYIADLMQAWLGILSRAKHTRSHEVIQETLSVRAQM TAILRRLNENG 130            140            150            160            170            180
<b>m993.pep</b>	190            200            210            220            230            240 ICRFHDLFNPQGAAYVVVNFI ALLELAKEGLV RIVQEDGFGEIRISLNHEGAHSDG I SG      :     :     :     :     :     :     :     :     :     :     :     :
<b>g993</b>	ICRFHALFNP EQGAAYVIVNFI ALLELAKEGLV GIVQEDGFGEIRISLNHEGAHSDG I FG 190            200            210            220            230            240
<b>m993.pep</b>	249 TRGGRDVFX      :
<b>g993</b>	TRGG RDVFX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3005>:

**a993.seq**

1	CTGAAAGTCG TATTGAGCAG TTTTCAAGGC CCTTTGGATC TGCTGCTCTA
51	CCTTATCCGC AAGCAGAACAA TCGATGTTCT CGATATTCCG ATGGTGAAGA
101	TTACCGAACAC GATCTGAC TACATCGCCC AAATAGAACAC CTATCAGTT
151	GATTGGCGG CGGAATATCT TTTGATGGCA GCAATGCTGA TTGAAATCAA
201	ATCGCGCTG CTGCTGCCGC GTACCGAACAC CGTCAAGAC GAAGAACCGC
251	ACCCCGCTGC CGAGTTGGTG CGCCGCCCTGC TGCTTACGA CGAGATGAAG
301	CTGGCGGCAC AAGGGTTGGA TGCCTTCCCT CGTGC GGAGATTTCGC
351	ATGGGCATAC CTGCCACTGG AAAATGCCCT CGAAGCCAG CTCCCCGAAG
401	TCTATATTAC CGACTTGACG CAGGC GTGAGTATTT GTCTCGGCA
451	AAACATACGC GCACCCACGA AGTTATCAA GAAACCATCT CCGTGC GCGC
501	GCAATGACG GCAATCCTGC GCCGTTGAA CAAACACGGG ATATG CAGGT
551	TTCAGGACCT GTTCAATCCC GAACAGGGCG CGGCTTACGT GGTGTCAC
601	TTCATCGCAC TGTTGGAGCT TGCCAAAGAA GGTTGGTCG GAATCGTACA
651	GGAAGTCGGT TTGGAGAAA TCCGAATCAG CCTCAATCAT GAGGGGGCGC
701	ATTCA GACGG CATTCCGGC ACACGGGGCG GGC GCGATGT GTCTAA

This corresponds to the amino acid sequence <SEQ ID 3006; ORF 993.a>:

**a993.pep**

1	LKVVLSSFQGPLDLLLLLIRKQNI DVL DIPMV KITEQYLHYIAQIETYQFDLAAEYLMA
51	DLAAEYLMA AMLIEIKSRL LPLRTEVDEEADPRAELV RRLLAYEQMK
101	LAAQGLDALP RAGRDFAWAY LPLEIAVEAK LPEVYITDLT QAWLSILSRA
151	KHTRSHHEVIK ETISVRAQM TAILRRLNKG ICRFHDLFNP EQGAAYVVVN
201	<u>FI ALLELAKE</u> GLVGIVQEVG FGEIRISLNH EG AHSDG I SG TRGRDVF*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 993 shows 97.6% identity over a 248 aa overlap with a predicted ORF (ORF 993) from *N. meningitidis*

**a993/m993** 97.6% identity in 248 aa overlap

<b>a993.pep</b>	10            20            30            40            50            60 LKVVLSFQGPLDLLLLLIRKQNI DVL DIPMV KITEQYLHYIAQIETYQFDLAAEYLMA      :     :     :     :     :     :     :     :     :     :     :
<b>m993</b>	LKVVLGSFQGPLDLLLLLIRKQNI DVL DIPMV KITEQYLHYIAQIETYQFDLAAEYLMA

	10	20	30	40	50	60
a993.pep	70	80	90	100	110	120
	AMLIEIKSRLLLPRTETVEDEEADPRAELVRRLLAYEQMKLAAQGLDALPRAGRDFAWAY					
m993	70	80	90	100	110	120
	AMLIEIKSRLLLPRTETVEDEEADPRAELVRRLLAYEQMKLAAQGLDALPRAGRDFAWAY					
a993.pep	130	140	150	160	170	180
	LPLEIAVEAKLPEVYITDLTQAWLSILSRAKHTRSHVIKETISVRAQMTAILRRLNKG					
m993	130	140	150	160	170	180
	LPLEIAVEAKLPEVYITDLTQAWLGILSPAKHTRSHVIKETISVRAQMTAILRRLNKG					
a993.pep	190	200	210	220	230	240
	ICRFHDLFNPQEQGAAYVVVNFIALLAKEGLVGVQEVGFGEIRISLNHEGAHSDGSG					
m993	190	200	210	220	230	240
	ICRFHDLFNPQGAAYVVVNFIALLAKEGLVRIVOEDGFGEIRISLNHEGAHSDGSG					
a993.pep	249					
	TRGGGRDVFX					
m993	249					
	TRGGGRDVFX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3007>:

**g996.seq**

1	ATGAACAGAA	GAACCTTCCT	CCTCGGGCGA	GGCGCGTTGC	TTCTTACCGC
51	CTGCGGCAGA	AAATCCGCC	GAACCCACGC	CAAATTC	GAAGGAAGCA
101	CCGTGCTTC	CTTGGCGAT	TCGCTCACCT	TCGGCTACGG	AGCAAACCC
151	GCGGAATCCT	ACCCCGCGCA	ACTGCAAAA	CTGACGGGTT	GGAATATTGT
201	CAACGGCGG	GTATCGGGCG	ATACGTCGC	GCAAGCCCTA	TCGCGCTGC
251	CCCGCCTGTT	GGCACGCAA	CCCAAGCTTG	TGATTGTCGG	CATAGGGCGC
301	AACGACTTTC	TGCGCAAAGT	TCCCAGGGAG	CAGACCCGGG	CCAATATCGC
351	GAAAATCATC	GAACCCGTGC	AAAAGGAAA	CATTCCCGCC	GTCCTCGTCG
401	GCGTGCCTGCA	CATCACACTG	GGCGCGTTG	TGCGGCATT	GAGCGACCAT
451	CCGCTGTATG	AGGATTGTC	CGAGGAATAC	GGCATTCCGT	TGTTCGGGCG
501	CGCGTGGCG	GAATTTGG	GCGATAATAA	TCTGAATTC	GACCAAATCC
551	ACGCCAACGG	CAAAGGCTAT	CGGAAATTG	CCGAAATTT	GAATCAATT
601	TTGAGAAAAC	ATGGGTTAG	ATAA		

This corresponds to the amino acid sequence <SEQ ID 3008 ORF 996.ng>:

**g996.pep**

1	MNRRTFLLGA	GALLTACGR	KSARTHAKIP	EGSTVLAGD	SLTFGYGANP
51	GESYPAQLQK	LTGWNIVNGG	VSGDTSAQAL	SRLPALLARK	PKLVIVGIGG
101	NDFLRKVPEE	QTRANIAKII	ETVQKENIPA	VLVGVPHTL	GALFGHLSDH
151	PLYEDLSEYY	GIPLFGGAWA	EILGNNNLKS	DQIHANGKGY	RKFAENLNQF
201	LRKHGFR*				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3009>:

**g996.seq**

1	ATGAACAGAA	GAACCTTCCT	CCTCGGGCGA	GGCGCGTTGC	TGCTTACCGC
51	CTGCGGCAGA	AAATCCGCC	GAACCCACGC	CAAATTC	GAAGGAAGCA
101	CCGTACTTTC	CTTGGCGAT	TCGCTCACCT	TCGGCTACGG	CGCAAACCC
151	GCGGAATCCT	ACCCCGCGCA	ACTGCAAAA	CTGACGGGTT	GGAATATTGT
201	CAACGGCGG	GTATCGGGCG	ATACATCTGC	CCAAGCCCTG	TCGCGCTGC
251	CCCGCCTGTT	GGCACGCAA	CCCAAGCTTG	TGATTGTCGG	CATAGGGCGC
301	AACGACTTTC	TGCGCAAAGT	TCCCAGGGAG	CAGACCCGGG	CCAATATCGC
351	GAAAATCATC	GAACCCGTGC	AAAAGGAAA	CATTCCCGCC	GTCCTCGTCG
401	GCGTGCCTGCA	CATCACACTG	GGTGCCTGTT	TGCGGCATT	GAGCGATCAT
451	CCGCTGTATG	AGGATTGTC	CGAGGAATAC	GGCATTCCGT	TGTTCGGGCG
501	CGCGTGGCG	GAATTTGG	GCGATAATAA	TCTGAATTC	GACCAAATCC
551	ACGCCAACGG	CAAAGGCTAT	CGGAAATTG	CCGAAAGATT	GAATCAATT
601	TTGAGAAAAC	AGGGGTTAG	ATAA		

This corresponds to the amino acid sequence <SEQ ID 3010, ORF 996>:

**g996.pep**

1	MNRRTFLLGA	GALLTACGR	KSARTHAKIP	EGSTVLAGD	SLTFGYGANP
51	GESYPAQLQK	LTGWNIVNGG	VSGDTSAQAL	SRLPALLARK	PKLVIVGIGG

101 NDFLRKVPKE QTRANIAKII ETVQKENIPA VLVGVPHITL GALFGHLSDH  
 151 PLYEDLSEEEY GIPLFGGAWA EILGDNNLKS DQIHANGKGY RKFAEDLNQF  
 201 LRKGFR

Computer analysis of this amino acid sequence gave the following results:  
Homology with a predicted ORF from *N. gonorrhoeae*

ORF 996 shows 98.1% identity over a 207 aa overlap with a predicted ORF (ORF 996) from *N. gonorrhoeae*

**m996/g996** 98.1% identity in 207 aa overlap

<b>m996.pep</b>	10            20            30            40            50            60 MNRRTFLLGAGALLTACGRKSARTHAKIPEGSTVLAGDSLTFGYGANPGESYPAOLQK        :     :     :     :     :     :     :     :     :     : 
<b>g996</b>	10            20            30            40            50            60 MNRRTFLLGAGALLTACGRKSARTHAKIPEGSTVLAGDSLTFGYGANPGESYPAOLQK 10            20            30            40            50            60
<b>m996.pep</b>	70            80            90            100            110            120 LTGWNIVNGGVSGDTSQAQLSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII        :     :     :     :     :     :     :     :     :     : 
<b>g996</b>	70            80            90            100            110            120 LTGWNIVNGGVSGDTSQAQLSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII 70            80            90            100            110            120
<b>m996.pep</b>	130            140            150            160            170            180 ETVQKENIPAVLVGVPHITL GALFGHLSDH PLYEDLSEEEY GIPLFGGAWAEILGDNNLKS        :     :     :     :     :     :     :     : 
<b>g996</b>	130            140            150            160            170            180 ETVQKENIPAVLVGVPHITL GALFGHLSDH PLYEDLSEEEY GIPLFGGAWAEILGDNNLKS 130            140            150            160            170            180
<b>m996.pep</b>	190            200 DQIHANGKGYRKFAEDLNQFLRKHGFR        :     : 
<b>g996</b>	190            200 DQIHANGKGYRKFAENLNQFLRKHGFRX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3011>:

**a996.seq**

1 ATGAAACAGAA GAACCTTCCT CCTCGGCGCA GGCCTGTTGC TCCTTACCGC  
 51 CTGGGGCAGA AAATCCGCCC GAACCCACCG CAAAATTCCC GAAGGAAGCA  
 101 CGCTACTTGC CTGGGGCGAT TCGCTTACCT TCGGCTACGG CGCAAACCCC  
 151 GCGGAATCTT ACCCCGCGCA ACTGCAAAAA CTGACGGGTT GGAATATTGT  
 201 CAACGGCGGC GTATCGGGCG ATACATCCGC CCAAGCCCTG TCGCCCTGTC  
 251 CCGCGCTGTGTT GGCACGCAAA CCCAAGCTTG TGATTGTCGG CATAGGGCGC  
 301 AACGACTTGC TGCGCAAAGT TCCCAAGGGAG CAGACCCGGG CCAATATCGC  
 351 GAAATATCATC GAAACCGGTGCA AGAAGGAAA CATCCCCGCC GTCCTCGTCG  
 401 GCGTGCCTGC CATTACCTTG GGCCTGTTGT TCGGGCATTT GAGCGATCAT  
 451 CCGCTGTATG AGGATTGTC CGAGGAATAC GGCATTCCGC TGTTCGGCGG  
 501 CGCGTGGGG GAAATTTTGG GCGATAATAA TCTGAAATCC GACCAATCC  
 551 ACGCCAACCG CAAAGGCTAT CGGAAATTG CCGAAGAGTTT GAATCAATT  
 601 TTGAGAAAAGGGTTTAG ATAA

This corresponds to the amino acid sequence <SEQ ID 3012; ORF 996.a>:

**a996.pep**

1 MNRRTFLLGA GALLTACGR KSARTHAKIP EGSTVLAGD SLTFGYGANP  
 51 GESYPAQLQK LTGWNIVNGG VSGDTSQAQL SRLPALLARK PKLVIVGIGG  
 101 NDFLRKVPKE QTRANIAKII ETVQKENIPA VLVGVPHITL GALFGHLSDH  
 151 PLYEDLSEEEY GIPLFGGAWA EILGDNNLKS DQIHANGKGY RKFAEDLNQF  
 201 LRKGFR\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 996 shows 100.0% identity over a 207 aa overlap with a predicted ORF (ORF 996) from *N. meningitidis*

**a996/m996** 100.0% identity in 207 aa overlap

<b>a996.pep</b>	10            20            30            40            50            60 MNRRTFLLGAGALLTACGRKSARTHAKIPEGSTVLAGDSLTFGYGANPGESYPAOLQK
-----------------	--

m996	MNRRTFLLGAGALLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPAQLQK					
	10	20	30	40	50	60
a996.pep	70	80	90	100	110	120
m996	LTGWNIVNGGVSGDTSQAQLSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII					
a996.pep	70	80	90	100	110	120
m996	LTGWNIVNGGVSGDTSQAQLSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII					
a996.pep	130	140	150	160	170	180
m996	ETVQKENIPAVLVGVPHITLGALFGHLSDHPLYEDLSEEEYGIPLFGGAWEILGDNNLKS					
a996.pep	130	140	150	160	170	180
m996	ETVQKENIPAVLVGVPHITLGALFGHLSDHPLYEDLSEEEYGIPLFGGAWEILGDNNLKS					
a996.pep	190	200				
m996	DQIHANGKGYRKFAEDLNQFLRKQGFRX					
a996.pep	190	200				
m996	DQIHANGKGYRKFAEDLNQFLRKQGFR					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3013>:

```

g997.seq (partial)
  1 ATGATGAACA CGCCGCATCC GCGCCCGAAA ATGCCGTCA TCGGCGCAGG
  51 CTGGCCGCGC TTGTCGGCGC CGTCACCTT GCGCGGCCAC CGCACGCTTA
 101 CCCCCTTTGA AGCGCCGGCG CAGGGGGCGA GAAAGGGCGC CACACTGGCC
 151 GGAATAACCGC ACGGTTTCGG TTTTTTGAC AACGGGCAGC ACATTTGCTT
 201 CGGCGCATAC CGGGCGTGT TGCGCTGTAT GAAAACCATC GCTTCAGACCC
 251 CCCGTGCGCG CTTTTTGCGC GTACCGCTGC ACTGGCATAT GCACGGCGGT
 301 TTGCACTTCC GCGCCCTCCC CCTGCGCGC CGCGTCGCA TTTGGGGGG
 351 CGTGTCTGG CGCCGGCGCG TACCGTCCGC ATTCAAAGCC AAACGTCTT
 401 CGCATATGTC CGATTGCGAG AAGTCCGCAC GCCTCGGACA GCGGACACGG
 451 ACAGTTGCAAC AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CGGCCGTAAT
 501 GCAGCTTTGG CAGGCCCTTG TCTGGGGCGC GCTCAACACG CCTTGGAAA
 551 CCGCAAGCCT CGCGTGTG TGCAACGTT TGTCCGACCG CGTGTGACG
 601 AAAATAACCGC GCGCGGACTA TCTCTTACCC AAACAGGATT TGGGCCAAT
 651 CGTCGCCGAA CCCGCTTGG CGGAGCTTCA ACGGCTCGGC CGGGACATCC
 701 GCCTCGAAAC GCGCGTATGC CGTCTGAACA CCCTCCCGGA CGGAAAAGTC
 751 CTCGTCACCG CGGAAGCCTT CGATGCCGC ATACTTGCCTA CGCGCCCTTA
 801 CCAGCCGGCG CGCGCTCTGC CGGAAGGCAC GCGGAACAC GTTCAGACGG
 851 CATATCAAAA CCTTCGCTAC CACGCCATCA CCACCGCTCA TCTGGCTCAT
 901 GCGGAACCCG TCCGCTGCG CGCCCCGCTG AccGGGATtg CCGAcggcAC
 951 ggcaCaaatG CTGCTTTGcc cgGGGCAGGC tccggactgc CcccaaAacg
1001 aagTCTCCGC cGTCAattgc GTTTCGAcc GCGtgcggcG Gtttgcaaa
1051 cgg...

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This corresponds to the amino acid sequence <SEQ ID 3014 ORF 997.ng>:

g997.pep (partial)  
1 MMNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTILFEAGR QAGGRARTLA  
51 GNTDGFGLD NGQHILLGAY RGVLRLMLKI GSDPRAAFKL VPLHWHMHGG  
101 LQFRALPLPA PLHILGGVLL ARRVPASAFKA KLLADMSDLR KSARLGQPD  
151 TVAQWLKORN VPRAAVMQFW QPLWVGALNT PLETASLRLV CNVLSGDVLT  
201 KKSGSDYLLP KQDLGAIVAE PALAELQRLG ADIRILETRVC RLNTLPDGKV  
251 LVNGEAFDAA ILATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLRY  
301 AEPVRLPAPL TGIADGTAQW LLCPGQAPDC PQNEVSAVIS VSDRVGAFAN  
351 R...

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 3015>:

```
m997.seq
 1 ATGATGAACA CGCGGCATCC GCGCCCGAAA ATCGCCGTCA TCGGCGCAGG
 51 CTGGGCAGGA CTGTCGGCCG CCGTCACCTT GGCGCGGCAC GCGGACGTTA
101 CCGCTTTGA AGCGCCGCGG CAGGGCGGCG GCAGGGCGC CACACTGGCC
151 GGAATATCCG ACGGTTGGAC TTTTTGGAC AACGGGCAGC ACATTTGCT
201 CGGGCATACT CGGGGGCTGT TGCGCCTGAT GAA:---TCATC GGTTCGGATC
251 CCCGTGCCGC CTTTTGGCGC GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTGCACTTCC GCGCCCTCCC CCTGCCCCGG CCGCTGCATA TTTTGGCGG
351 CCGTCTGCTG GCGGGCGCTG CACCGACTGC ATTCAAAGCC AAACCTGCTTG
401 CGGATATGTC CGATTGGCA AAGTCGGCAG GCCTCCGGAC GCGCCGACAGC
451 AAGCTGGCCG AATGCGCTGAA ACAGCGGAAC GTGCCGGCTG CGCCGGTGTAT
501 GCAGTTTGG CAGCCCTGG TTTGGGGCGC GCTCAACACG CTTTGTGAAA
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551 CGCGCAAGCCT GCGCGTGTG TGCAACGTT TGTCCGACGG CGTGCTGACG
601 AAAAAATCCG GCAGCGACTA TCTCCTACCC AAGCAGGATT TGGGCGCAAT
651 CGTCGCCGAA CCCGCCCTTG CGGATCTTCA ACGGCTCGGC GCGGACATCC
701 GCCTCGAAAC CGCGGTATGCC CGCTCTGAACA CCCTCCCGGA CGGAAAGTG
751 CTCGTCACCG GCGAAGCTTT CGATGCCGCC GTCCCCGCCA CGGGCCCTA
801 CCACGCCGCC CGCCTCCTGC CGAAGGCAC GCGCAACAC GTTCAGACGG
851 CATATCAAAA CCTTGGCTAC CACGCCATCA CCACCGCTCA TCTGCGCTAC
901 GCGGAACCC CGCGCTGCC CGGGCCGCTG ACCGGGCTTG CGGACGGCAC
951 GTGCAATGG CTGCTTTGCC GGGGCAGGCT CGGACTGCCT GAAAACGAAG
1001 TGCCCGCGT CATAGCGTT TCCGACCGCG TCAGCGCTT TGCAACCGG
1051 GCGTGGGCGG ACAAGCCCA CGCCGACCTC AAACGATCC TTCCGCAATT
1101 GGGCGAACCC GAAGCCGTGC CGCTCATCAC CGAAAACGC GCGACACCG
1151 CAGCCGATGC TCCGCCGCCG GACTTGTGCTG GTTGCACCCG GCACCGCATC
1201 TCCCGCCGCC GCGACTACCT CCACCCGGAC TACCCGCCA CGCTCGAAGC
1251 CGCCGTACAA TCAGGTTTCG CGTCGGCGGA AGCCTGCCTG CAAAGCTGA
1301 GCGATGCCGT CTGA

```

This corresponds to the amino acid sequence <SEQ ID 3016; ORF 997>:

**m997.pep**

```

1 MMNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTLFEARQ QAGGRARTLIA
51 GNTDGFGLD NQGHILLGAY RGVLRLMKTI GSDPRAAFLRL VPLHWHMHGG
101 LQFRALPLPA PLHILGGVLL ARRAPTAFFKA KLLADMSDLO KSARLGQPDPT
151 TVAQWLQORN VPRAAVMFOFW QPLVWGAINT PLETASLRLV CNVLSDGVL
201 KKSQSDYLLP KQDLGAIVAE PALADLQRLG ADIRLETRVC RLNTLPDGKV
251 LVNGEAFDAA VPATAPYHAA ALIPEGTPEH VQTAQNLRY HAITTVYLRY
301 AEPVRLPAPL TGLADGTVQW LLCRGRGLP ENEVSAVISV SDRVGAFA
351 AWADKAHADL KRILPHLGEPE EAVRVITEKR ATTAADAPP DLSWLHRHRI
401 FPAGDYLHPD YPATLEAAVQ SGFASAEACL QSLSDAV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 997 shows 96.0% identity over a 351 aa overlap with a predicted ORF (ORF 997) from *N. gonorrhoeae*

**g997/m997 96.0% identity in 351 aa overlap**

	10	20	30	40	50	60	
g997.pep	MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLFEARQAGGRARTLAGNTDGFGLD	:     :     :     :     :     :     :     :     :     :     :	:     :     :     :     :     :     :     :     :     :     :	:     :     :     :     :     :     :     :     :     :     :	:     :     :     :     :     :     :     :     :     :     :	:     :     :     :     :     :     :     :     :     :     :	
m997	MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLFEARQAGGRARTLAGNTDGFGLD	10	20	30	40	50	60
g997.pep	NGQHILLGAYRGVRLRMLKTIGSDPRAAFLRLVPLHWHMHGGLQFRALPLPAPLHILGGVLL	70	80	90	100	110	120
m997	NGQHILLGAYRGVRLRMLKTIGSDPRAAFLRLVPLHWHMHGGLQFRALPLPAPLHILGGVLL	70	80	90	100	110	120
g997.pep	ARRVPSAFKAKLLADMSDLOQKSARLQDQPTTVAQWLKQQRNVPRAAVMQFWQPLVWGA	130	140	150	160	170	180
m997	ARRAPTAFFKAQKLLADMSDLOQKSARLQDQPTTVAQWLKQQRNVPRAAVMQFWQPLVWGA	130	140	150	160	170	180
g997.pep	PLETASLRLCNVLSDGVLTKKSGSDYLLPKQDLGAIVAEPALAELQRLGADIRLETRVC	190	200	210	220	230	240
m997	PLETASLRLCNVLSDGVLTKKSGSDYLLPKQDLGAIVAEPALADLQRLGADIRLETRVC	190	200	210	220	230	240
g997.pep	RLNTLPDGKVLVNGEAFDAAVATAPYHAAALLPEGTPEH VQTAQNLRY HAITTVYLRY	250	260	270	280	290	300
m997	RLNTLPDGKVLVNGEAFDAAVATAPYHAAALLPEGTPEH VQTAQNLRY HAITTVYLRY	250	260	270	280	290	300
g997.pep	AEPVRLPAPLTGIADGTAQWLLCPGQAPDCPQNEVSAVISVSDRVGAFA	310	320	330	340	350	
m997	AEPVRLPAPLTGLADGTVQWLLCRGRL-GLPENEVSAVISVSDRVGAFA	310	320	330	340	350	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3017>:

**a997.seq**

```

1  ATGATGAACA CGCCGCATCC GCGCCCGAAA ATCGCCGTCA TCGGCCGAGG
51  CTGGGCCGGC TTGTCCGCCG CCGTTACCTT GGCGCGGCAC GCCGACGTTA
101 CCCTGTTGA AGCCCGGCCGG CAGCCGGGGC GCAGGGCGGG CGCACTGGCC
151 GGAATACCGC ACGGTTTCGG TTTTTGGAC AACGGGCAGC ATATTTACT
201 CGGCCATAC CGGGGGCGTGT TGGCCCTGAT GAAACACATC GGTTCAGACC
251 CCCATGCCGC CTTTTGCGC GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTGCAAGTCTT CGCGCCCTCCC CCTGCCCGGG CCCTGCTATA TTTTGGGGGG
351 CGTGTGCTT ATTCAAAGCC AAACGTGCTTG
401 CGGATATGTC CGATTTGCAG AAGTCGCAAC GCCTCGGACA GCCCGACAGG
451 ACAGTGGCGC AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CCGCGCTAAT
501 GCAGTTTGG CAGCCCTTGG TTTGGGGCGC GCTAACACAGG CTTTGGAAA
551 CGCGAACCTT TGCAACAGTT TGTCGGACGG CGTGCTGACG
601 AAAAATCCG GCAGGGACTA TCTCTTACCC AAACAGGATT TGGGGCAAT
651 CGTCGCCGA CCGCCCTTGC CGGAGCTTCA ACGGCTCGGC CGGGACATCC
701 GCCTCGAAAC GCGCATATGC CGTCTGAACA CCTCCCGGA CGGGAAAGTG
751 CTCGTCAACCGC GCGAACCTT CGATGCCGC GTCGCCGCATA CGCGCCCTA
801 CGACGCCGC CGCGCTCTGC CGAAGGACAC GCGCAACAC GTTCAGACGG
851 CATATCAAA CCTTCGCTAT CACGCCATCA CCACCGCTTA TCTTCGCTAT
901 GCCGAACCCG TCCGCTTGCC TGCCCCGCTG ACCGGACTTG CCGACGGAC
951 GTGCAATGG CTGCTTTGCC GGGGAGGCT CGGACTGCTT GAAARCGAAAG
1001 TGTCGGCGT CATACGGCTT TCCGACCGGC TGCGCGCTT TGCAAACCGG
1051 CGCGTGGCGC ACAAAGTTCA CGCGGACCTC AAACGCATCC TTCCGCTT
1101 GGGCGAACCC GAAGCCGTGC CGGTCACTCAC CGAAAAACCC GCCACAACCG
1151 CAGCCGATGC CCGCCGGCCG GATTGTCGT GTTGCACCG GCACCGCATC
1201 TTCCCGCCGAC GCGACTACCT CCACCCAGAC TACCCCGCCA CGCTCGAAGC
1251 CGCCGTACAA TCAGGTTTCG CGTCGGCGGA AGCTGCCCTG CAAAGCTGA
1301 GCGATGCCGT CTGA

```

This corresponds to the amino acid sequence <SEQ ID 3018; ORF 997.a>:

**a997.pep**

```

1  MMNTPHPRKIAVIGAGWAGLSAAVTLARHADVTLFEAGRQAGGRALA
51  GNTDGFGLD NGQHILLGAY RGVLRLMKTI GSDPHAAFLR VPLWHMHCG
101 LQFRALPLPA PLHILGGVLL ARRVPASAFKA KLLADMSDLQ KSARLGQPDT
151 TVAQWLKQRN VPRAAVMQFW QPLVWGAINT PLETASLRVL CNVLSDGVL
201 KKSGSDYLLP KQDLGAIVAE PALAELORLG ADIRLETRIC RLNTLPDGKV
251 LVNGEPFDAA VPATAPYHAA ALLEPGTPEH VOTAYQNLRY HAITTVYI
301 AEPVRLPAPL TGLADGTVQW LLCRGRLGLP ENEVSAVISV SDRVGAFA
351 AWADKVKHADL KRILPHLGEPE AVAVRIVITEKR ATTAADAPP DLSWLHRHRI
401 FPAGDYLHPD YPATLEAAVQ SGFASAEACL QSLDAV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 997 shows 98.2% identity over a 437 aa overlap with a predicted ORF (ORF 997) from *N. meningitidis*

**a997/m997 98.2% identity in 437 aa overlap**

	10	20	30	40	50	60
a997.pep	MMNTPHPRKIAVIGAGWAGLSAAVTLARHADVTLFEAGRQAGGRALA	LAGNTDGFGFLD				
m997	MMNTPHPRKIAVIGAGWAGLSAAVTLARHADVTLFEAGRQAGGRARTL	AGNTDGFGFLD				
	10	20	30	40	50	60
	70	80	90	100	110	120
a997.pep	NGQHILLGAYRGVLRLMKTI	GSDPHAAFLRVPLHWHMHGGLQFRALPLPAPLHILGGVLL				
m997	NGQHILLGAYRGVLRLMKTI	GSDPRAAFLRLPVLHWHMHGGLQFRALPLPAPLHILGGVLL				
	70	80	90	100	110	120
	130	140	150	160	170	180
a997.pep	ARRVPSAFKAKLLADMSDLQKSARLGQPD	TTVAQWLQQRNVPRAAVMQFWQPLVWGAINT				
m997	ARRAPTAFKAKLLADMSDLQKSARLGQPD	TTVAQWLQQRNVPRAAVMQFWQPLVWGINT				
	130	140	150	160	170	180
	190	200	210	220	230	240
a997.pep	PLETASLRVL	CNVLSDGVLTKSGSDYLLPKQDLGAIVAEPALAELORLGADIRLETRIC				
	190	200	210	220	230	240

m997	PLETASLRVLCNVLSDGVLTKSGSDYLLPKQDLGAIVAEPALADLQLRGADIRLETRVC
	190 200 210 220 230 240
	250 260 270 280 290 300
a997.pep	RLNTLPDGKVLVNGEFPDAAVPATAPYHAAALLPEGTEPEHVQTAYQNLRYHAITTVYLYR      :     :     :     :     :     :     :     :     :     :     :     :
m997	RLNTLPDGKVLVNGEAFDAAVPATAPYHAAALLPEGTEPEHVQTAYQNLRYHAITTVYLYR
	250 260 270 280 290 300
	310 320 330 340 350 360
a997.pep	AEPVRLPAPLTGLADGTQWLLCRGRGLPENEVSAVISVSDRVGAFAFANRAWADKVHADL      :     :     :     :     :     :     :     :     :     :     :     :
m997	AEPVRLPAPLTGLADGTQWLLCRGRGLPENEVSAVISVSDRVGAFAFANRAWADKAHADL
	310 320 330 340 350 360
	370 380 390 400 410 420
a997.pep	KRILPHLGEPEAVRVITEKRATTAADAPPDLSWLHRHRIFPAGDYLHPDYPATLEAAVQ      :     :     :     :     :     :     :     :     :     :     :     :
m997	KRILPHLGEPEAVRVITEKRATTAADAPPDLSWLHRHRIFPAGDYLHPDYPATLEAAVQ
	370 380 390 400 410 420
	430
a997.pep	SGFASAEACLQSLSDAVX      :     :     :
m997	SGFASAEACLQSLSDAVX
	430

**g999.seq** Not found yet

**g999.pep** Not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3019>:

m999.seq	1 ATGAATATGA AAAAATTGAT TTCCGCAATT TGTGTTTCAA TTGTTTTATC
	51 AGCCTGCAAC CAAACATCAA AAAC       AGC   AAGA CCTGTCCAAA
101	GTATCCAGGC TGCTGATTGT ACCGGCCCAA TGGACATCAC AGTTGAACAA
151	TATCTCATCA ATTTGGAGCA AGCATTAAAA ACTCAGAACG TCTCAACAAA
201	AATCCATAAT AAAAATATTG TCAAGACCGA TTGTGGTTAT GACCTTACTT
251	TGTTAATGGA TTTGGGGCG ATTGCGCTCA AACTGGACGA GCAGCAAAAA
301	ATTAGAGCTA TCTCAGTAGG CTACATTTTA AAAACCGACG GAGAGAAAGG
351	ACAAAATCTA GTCAATAATG CCATAAATGG ATTACACAGT ATTCAAGGAG
401	TTCTGTCTTT AACTACCACA GACAAATTGG GCGAATCCGA AGCAGGAAAA
451	CAACTTTTA CAGCTTTAAC CGAAGTCGTC AAAGAAATCCA ATCAGACAGG
501	AGCAACAGCG CAAAAGACG TTCCGGCAGA TGGTATTAA TATAGCGTTG
551	TTTTGAAAA AGAACAAAC ACCATTGCAA TAATCGGCAG AAAACAAACCC
601	TAA

This corresponds to the amino acid sequence <SEQ ID 3020; ORF 999>:

m999.pep	1 MNMKKLISAI CVSIVLSCACN QQSCTAQAEV PVQSIQAADC TAPMDITVEQ
	51 YLINLEQAFK TQNVSTKIHN KNIVKTDGCV DLTLMDFGA IALKLDEQQK
101	IRAIISVGYL KTDGEKGQNL VNNAINGLHS IQAVLSLTTE DKLGESEAGK
151	QLFTALTEVV KESNQTGATA QKDVPADGIL YSVVFEKETN TIAIIGRKQP

**a999.seq** Not found yet

**a999.pep** Not found yet

The foregoing examples are intended to illustrate but not to limit the invention.

## CLAIMS

1. A protein comprising a fragment of an amino acid sequence from SEQ ID 2790 wherein said fragment comprises at least 7 amino acids from said sequence.
2. A protein comprising an amino acid sequence selected from the group consisting of even numbered SEQ IDs from SEQ ID number 2 through SEQ ID number 3020.
3. A protein having 50% or greater homology to a protein according to claim 1.
4. A protein comprising a fragment of an amino acid sequence selected from the group consisting of even numbered SEQ IDs from SEQ ID number 2 through SEQ ID number 3020, wherein said fragment comprises 7 or more consecutive amino acids from said sequence.
5. An antibody which binds to a protein according to any one of claims 1 to 3.
6. A nucleic acid molecule which encodes a protein according to any one of claims 1 to 3.
7. A nucleic acid molecule according to claim 5, comprising a nucleotide sequence selected from the group consisting of odd numbered SEQ IDs from SEQ ID number 1 through SEQ ID number 3019.
8. A nucleic acid molecule comprising a fragment of a nucleotide sequence selected from the group consisting of odd numbered SEQ IDs from SEQ ID number 1 through SEQ ID number 3019, wherein said fragment comprises 10 or more consecutive nucleotides from said sequence.
9. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 5.
10. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 6.
11. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 7.
12. A composition comprising a protein, a nucleic acid molecule, or an antibody according to any preceding claim.
13. A composition according to claim 11 being a vaccine composition or a diagnostic composition.
14. A composition according to claim 11 for use as a pharmaceutical.
15. The use of a composition according to claim 11 in the manufacture of a medicament for the treatment or prevention of infection due to Neisserial bacteria.

16. A composition comprising a protein of claim 1 wherein said composition is immunogenic.

17. A composition comprising a protein of claim 2 wherein said composition is immunogenic.

18. A composition comprising a protein of claim 3 wherein said composition is immunogenic.

09/674546

WO 99/57280

1/30

PCT/US99/09346

279 (10.5 kDa)

Fig. 2

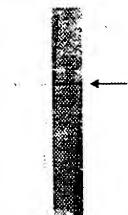
A) PURIFICATION

M1 279

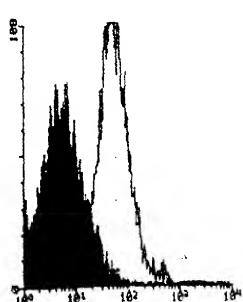


B) WESTERN BLOTH

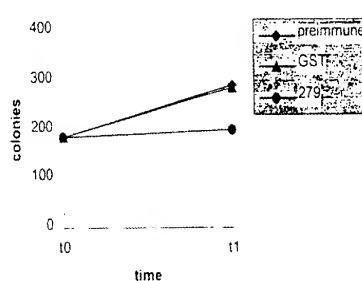
TP OMV



C) FACS



D) BACTERICIDAL ASSAY



E) ELISA assay: positive

279

The predicted gene 279 was cloned in pGex vector and expressed in *E. coli*. The product of protein expression and purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 279-GST purification. Mice were immunized with the purified 279-GST and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that protein 279 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B)

## 576 (27.8 kDa)

Fig. 3

## A) PURIFICATION

M1 576



## B) WESTERN BLOTH

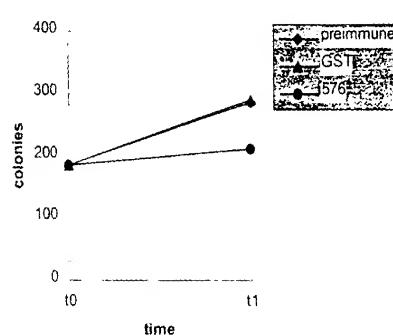
TP OMV



## C) FACS



## D) BACTERICIDAL ASSAY



## E) ELISA assay: positive

## 576

The predicted gene 576 was cloned in pGex vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 576-GST fusion protein purification. Mice were immunized with the purified 576-GST and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 576 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

## 519 (33 kDa)

## A) PURIFICATION

M1 519

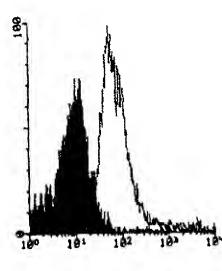


## B) WESTERN BLOTH

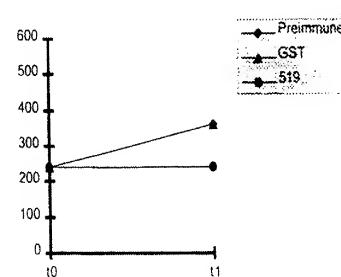
TP OMV



## C) FACS



## D) BACTERICIDAL ASSAY

E) ELISA assay: positive

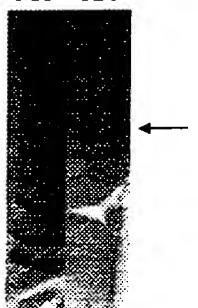
## 519

The predicted gene *519* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 519-His fusion protein purification. Mice were immunized with the purified 519-His and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 519 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

## 121 (40 kDa)

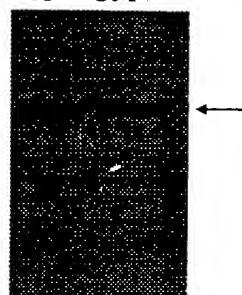
## A) PURIFICATION

M1 121

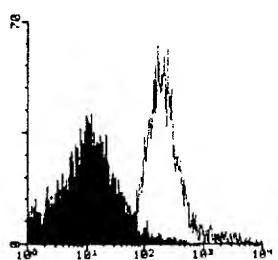


## B) WESTERN BLOTH

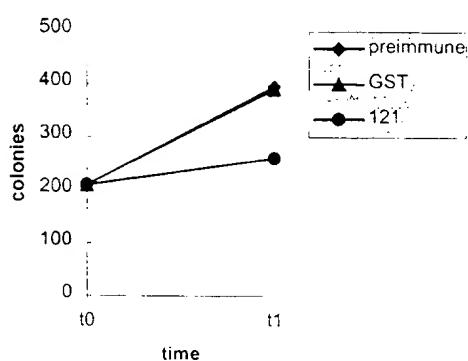
TP OMV



## C) FACS



## D) BACTERICIDAL ASSAY

E) ELISA assay: positive

## 121

The predicted gene *121* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 121-His fusion protein purification. Mice were immunized with the purified 121-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 121 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

Fig. 5

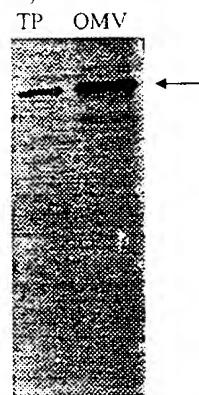
128 (101 kDa)

Fig. 6

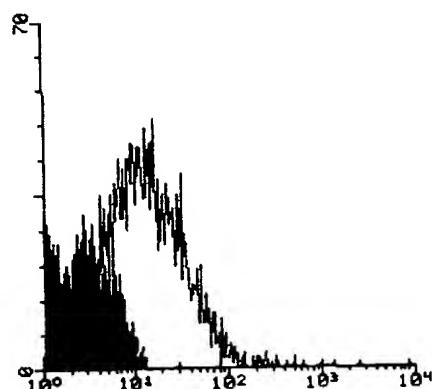
## A) PURIFICATION



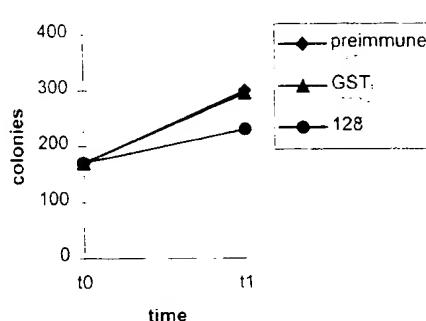
## B) WESTERN BLOTH



## C) FACS



## D) BACTERICIDAL ASSAY



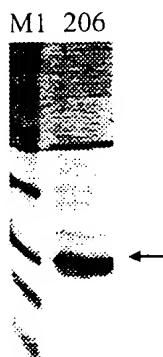
## E) ELISA assay: positive

128

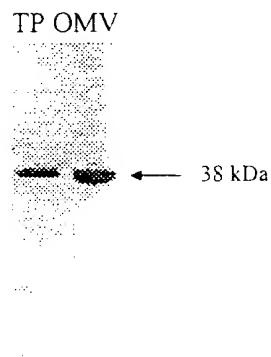
The predicted gene 128 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 128-His purification. Mice were immunized with the purified 128-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D) and ELISA assay (panel E). Results show that 128 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

Fig. 7

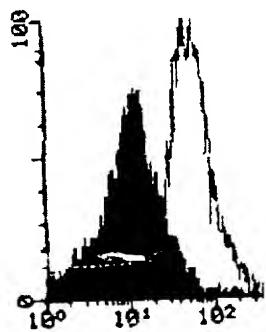
## A) PURIFICATION



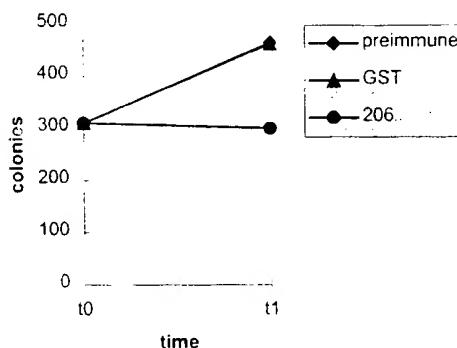
## B) WESTERN BLOTH



## C) FACS



## D) BACTERICIDAL ASSAY



## E) ELISA assay: positive

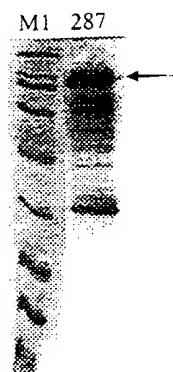
## 206

The predicted gene 206 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 206-His purification. Mice were immunized with the purified 206-His and sera were used for Western blot analysis (panel B). It is worthnoting that the immunoreactive band in protein extracts from meningococcus is 38 kDa instead of 17 kDa (panel A). To gain information on the nature of this antibody staining we expressed ORF 206 in *E. coli* without the His-tag and including the predicted leader peptide. Western blot analysis on total protein extracts from *E. coli* expressing this native form of the 206 protein showed a recative band at a position of 38 kDa, as observed in meningococcus. We conclude that the 38 kDa band in panel B) is specific and that anti-206 antibodies, likely recognize a multimeric protein complex. In panel C is shown the FACS analysis, in panel D the bactericidal assay, and in panel E) the ELISA assay. Results show that 206 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

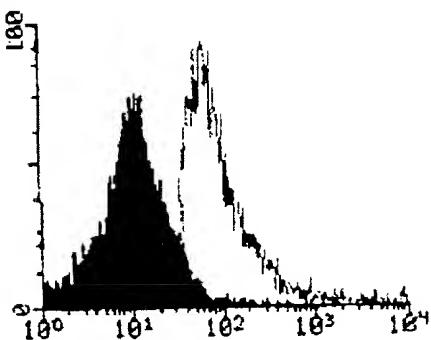
287 (78 kDa)

Fig. 8

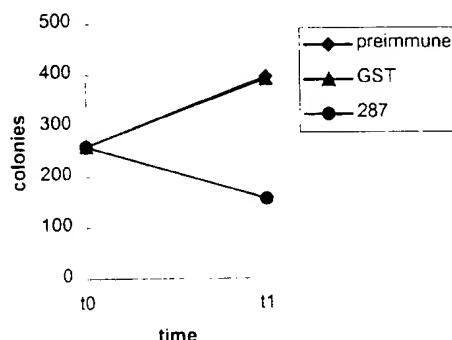
## A) PURIFICATION



## B) FACS



## C) BACTERICIDAL ASSAY

D) ELISA assay : positive

## 287

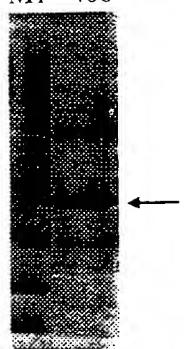
The predicted gene 287 was cloned in pGex vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 287-GST fusion protein purification. Mice were immunized with the purified 287-GST and sera were used for FACS analysis (panel B), bactericidal assay (panel C), and ELISA assay (panel D). Results show that 287 is a surface-exposed protein. Symbols: M1, molecular weight marker. Arrow indicates the position of the main recombinant protein product (A).

406 (33 kDa)

Fig. 9

## A) PURIFICATION

M1 406

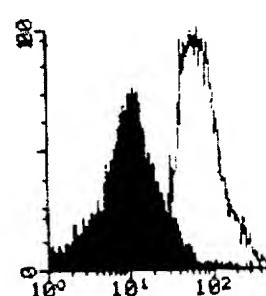


## B) WESTERN BLOTH

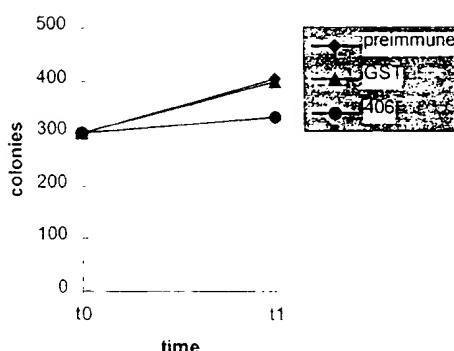
TP OMV



## C) FACS



## D) BACTERICIDAL ASSAY

E) ELISA assay : positive

## 406

The predicted gene 406 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 406-His fusion protein purification. Mice were immunized with the purified 406-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 406 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

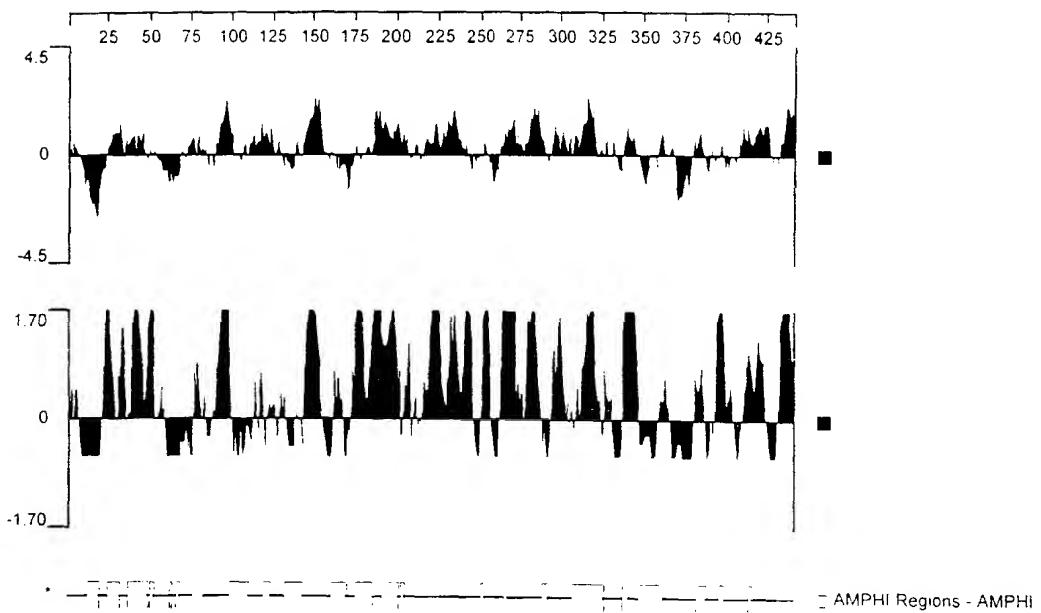
Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 10

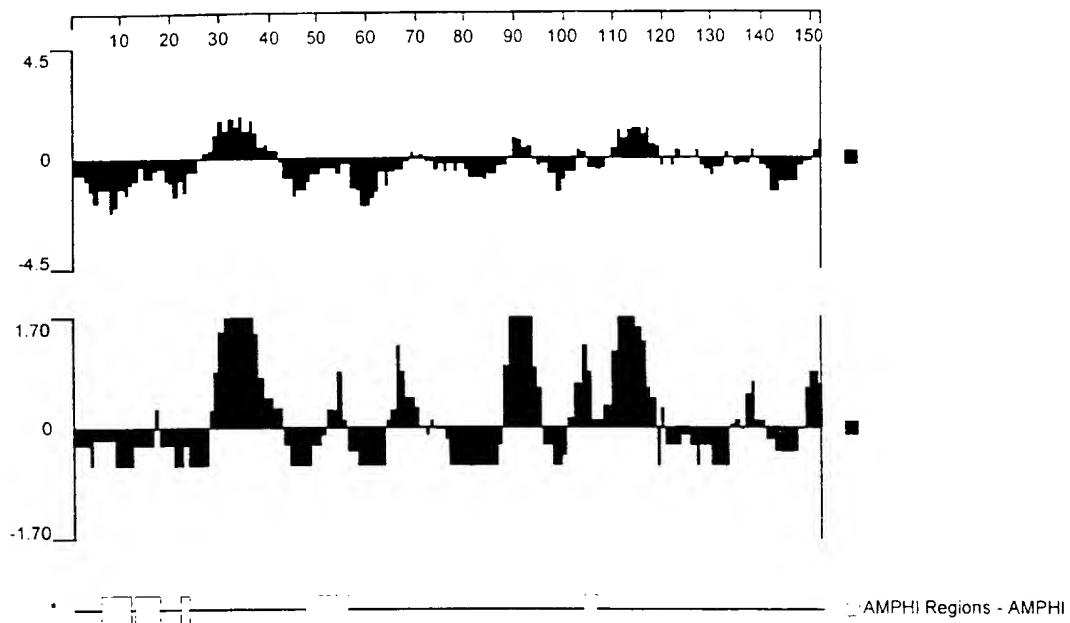
Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 11

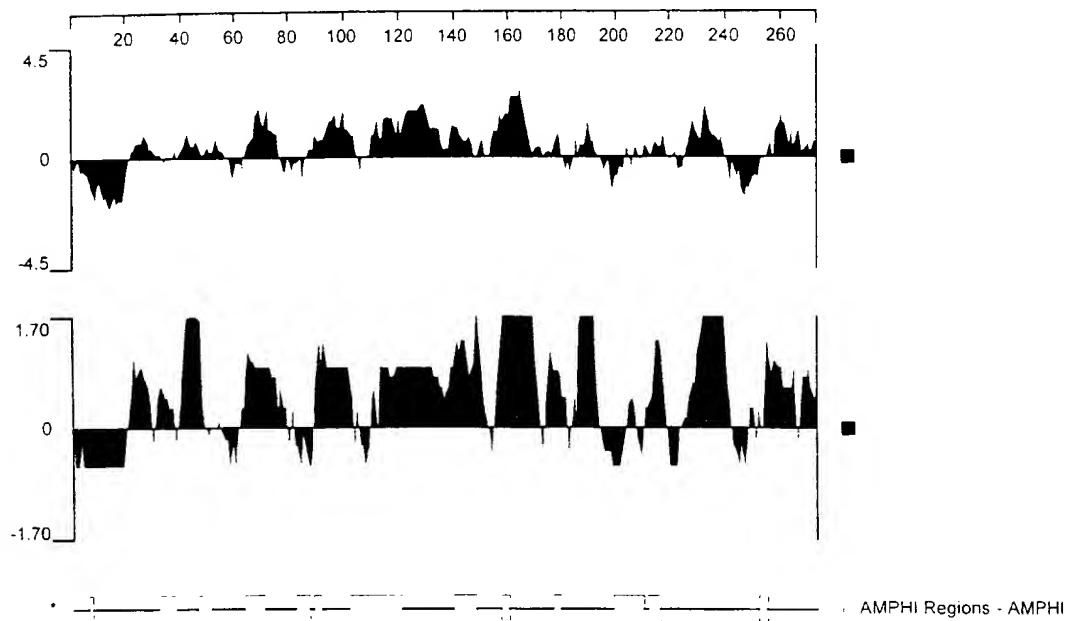
11/30  
576-1Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 12

09/674546

WO 99/57280

PCT/US99/09346

12/30  
519-1

Hydrophilicity Plot, Antigenic Index and AMPHI Regions

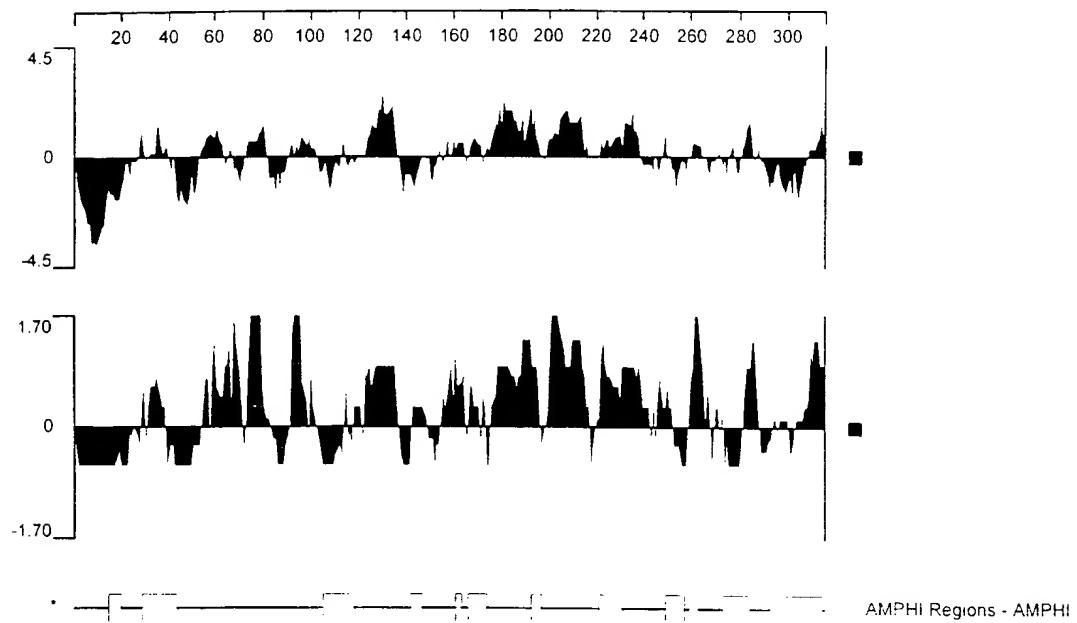


Fig. 13

09/674546

WO 99/57280

13/30

PCT/US99/09346

121-1

Hydrophilicity Plot, Antigenic Index and AMPHI Regions

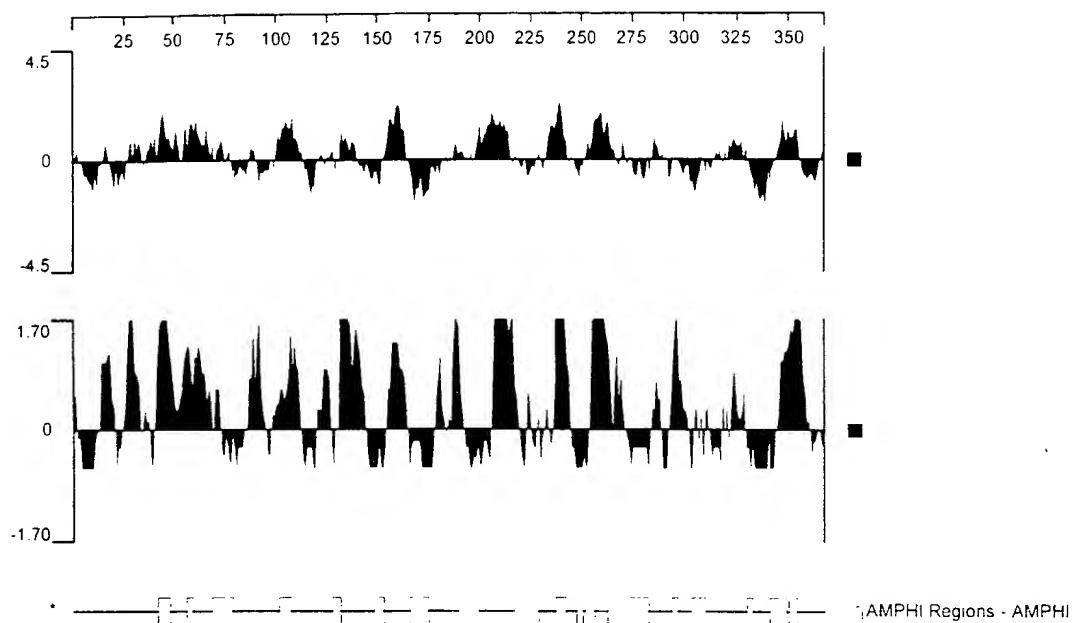


Fig. 14

09/674546

WO 99/57280

PCT/US99/09346

14/30

128-1

Hydrophilicity Plot, Antigenic Index and AMPHI Regions

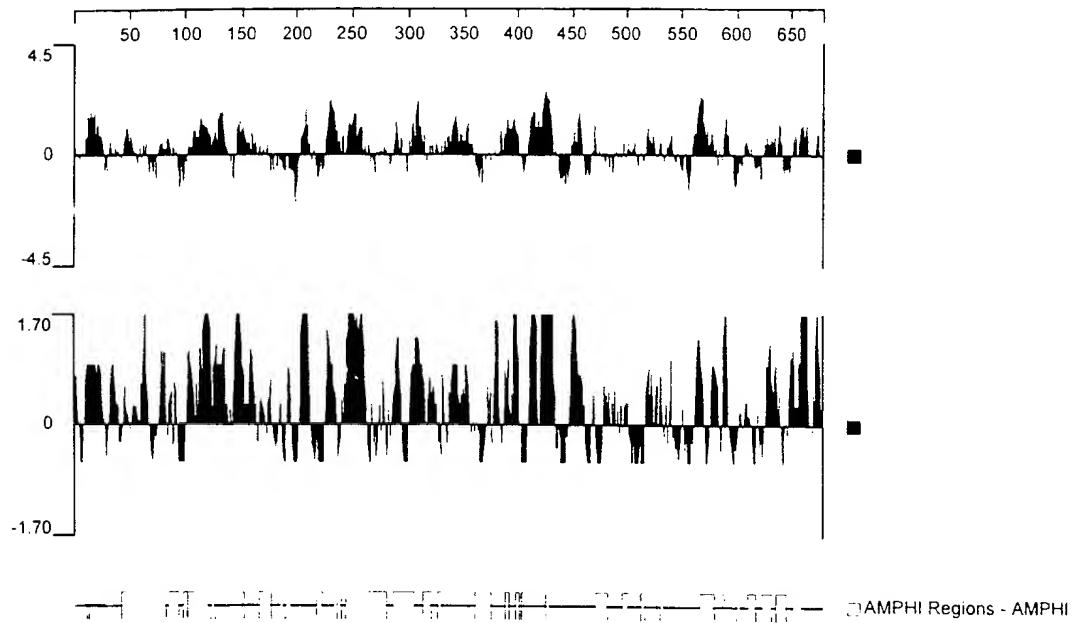


Fig. 15

09/674546

WO 99/57280

15/30

PCT/US99/09346

206

Hydrophilicity Plot, Antigenic Index and AMPHI Regions

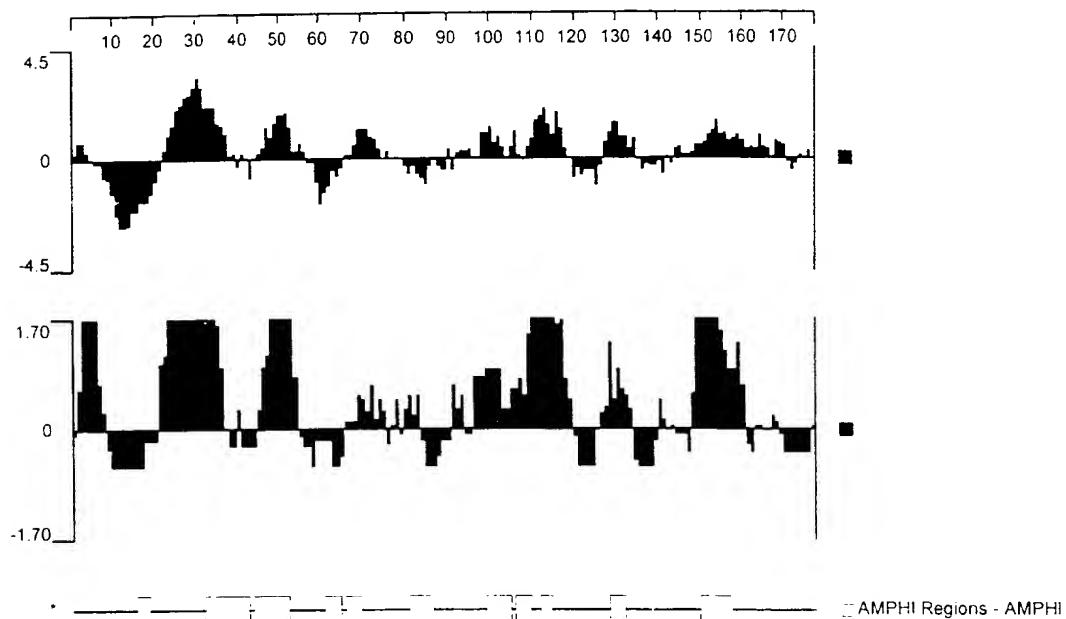


Fig. 16

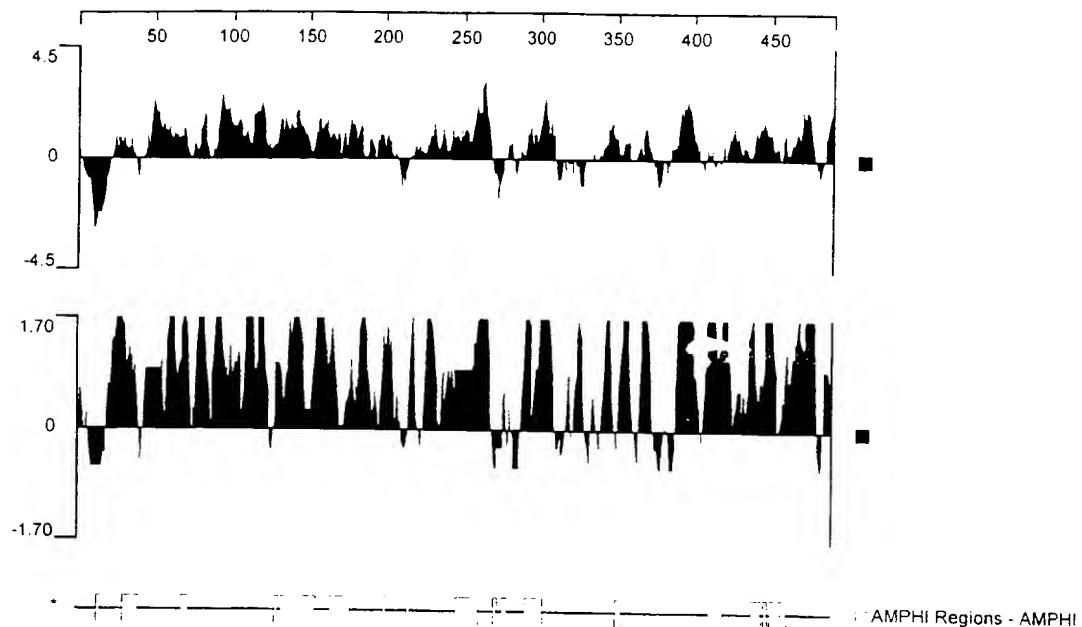
Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 17

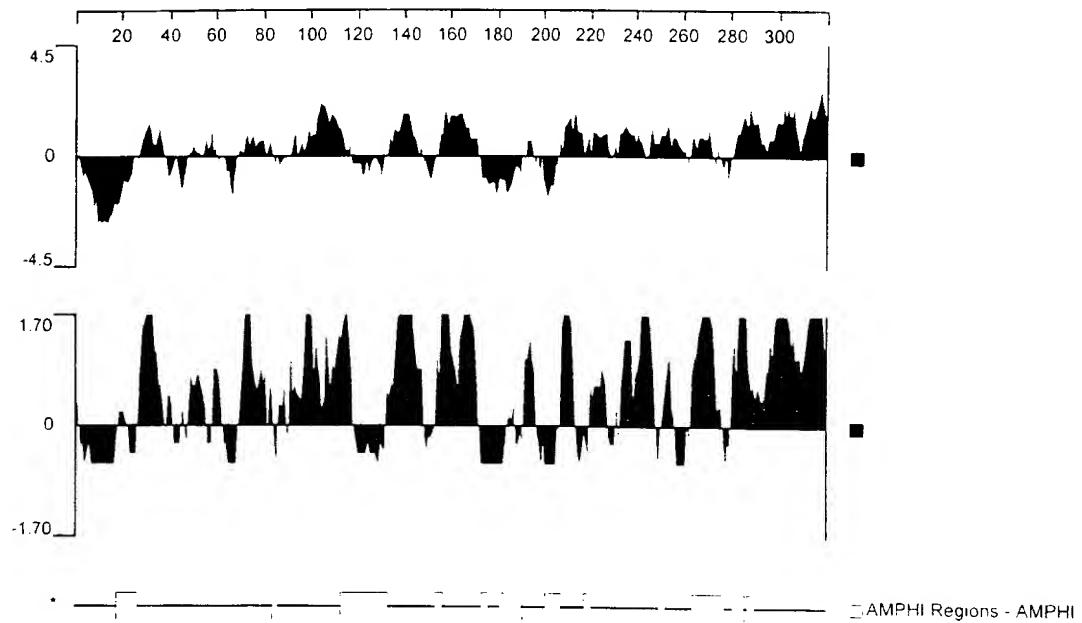
Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 18

zo05_225	1	MDSFFKPAVWAFLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG
zo08_225	1	MDSFFKPAVWAFLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG
z2491	1	MDSFFKPAVWAFLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG
zo11_225	1	MDSFFKPAVWAFLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG
zo20_225	1	MDSFFKPAVWAFLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG
zo01_225	1	MDSFFKPAVWAFLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG
zo09_225	1	MDSFFKPAVWAFLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG
zo12_225	1	MDSFFKPAVWAFLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG
zo22_225	1	MDSFFKPAVWAFLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG
zo23_225	1	MDSFFKPAVWAFLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG
zo24_225	1	MDSFFKPAVWAFLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG
zo25_225	1	MDSFFKPAVWAFLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG
zo26_225	1	MDSFFKPAVWAFLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG
zo96_225	1	MDSFFKPAVWAFLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG
zo02_225	1	MDSFFKPAVWAFLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG
zo04_225	1	MDSFFKPAVWAFLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG
zo06_225	1	MDSFFKPAVWAFLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG
zo07_225	1	MDSFFKPAVWAFLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG
zo10_225	1	MDSFFKPAVWAFLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG
zo14_225	1	MDSFFKPAVWAFLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG
zo16_225	1	MDSFFKPAVWAFLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG
zo17_225	1	MDSFFKPAVWAFLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG
zo18_225	1	MDSFFKPAVWAFLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG
zo19_225	1	MDSFFKPAVWAFLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG
zo21_225	1	MDSFFKPAVWAFLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG
zo27_225	1	MDSFFKPAVWAFLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG
zo28_225	1	MDSFFKPAVWAFLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG
zo29_225	1	MDSFFKPAVWAFLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG
zo13_225	1	MDSFFKPAVWAFLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG
zo03_225	1	MDSFFKPAVWAFLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG
zo15_225	1	MDSFFKPAVWAFLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG
fa1090	1	MDSFFKPAVWAFLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG
zo32_225	1	MDSFFKPAVWAFLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG
zo33_225	1	MDSFFKPAVWAFLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG
zo05_225	61	NADELIGSAMGLNE.....
zo08_225	61	NADELIGSAMGLNE.....
z2491	61	NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGSAMGLNEQPVLPVNRVPARRAGNA
zo11_225	61	NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGSAMGLNEQPVLPVNRVPARRAGNA
zo20_225	61	NADELIGSAMGLNEQPVLPINRAPARRAGNADELIGSAMGLNEQPVLPVNRVPARRAGNA
zo01_225	61	NADELIGSAMGLNE.....
zo09_225	61	NADELIGSAMGLNE.....
zo12_225	61	NADELIGSAMGLNE.....
zo22_225	61	NADELIGSAMGLNE.....
zo23_225	61	NADELIGSAMGLNE.....
zo24_225	61	NADELIGSAMGLNF.....
zo25_225	61	NADELIGSAMGLNF.....
zo26_225	61	NADELIGSAMGLNF.....
zo96_225	61	NADELIGSAMGLNF.....
zo02_225	61	NADELIGSAMGLNF.....
zo04_225	61	NADELIGSAMGLNF.....
zo06_225	61	NADELIGSAMGLNF.....
zo07_225	61	NADELIGSAMGLNF.....
zo10_225	61	NADELIGSAMGLNF.....
zo14_225	61	NADELIGSAMGLNF.....
zo16_225	61	NADELIGSAMGLNF.....
zo17_225	61	NADELIGSAMGLNF.....
zo18_225	61	NADELIGSAMGLNF.....
zo19_225	61	NADELIGSAMGLNF.....
zo21_225	61	NADELIGSAMGLNF.....
zo27_225	61	NADELIGSAMGLNF.....
zo28_225	61	NADELIGSAMGLNF.....
zo29_225	61	NADELIGSAMGLNF.....
zo13_225	61	NADELIGSAMGLNF.....
zo03_225	61	NADELIGSAMGLNF.....
zo15_225	61	NADELIGSAMGLNF.....
fa1090	61	NADELIGSAMGLNF.....
zo32_225	61	NADELIGSAMGLNF.....
zo33_225	61	NADELIGSAMGLNF.....

Fig. 19A

zo05_225	92	DELIGSAMGLNEQPVLVPNRAPIRAGNADELIGNAMGLLGIAYRYGGTS	STGFDCSGF
zo08_225	92	DELIGSAMGLNEQPVLVPNRAPIRAGNADELIGNAMGLLGIAYRYGGTS	STGFDCSGF
z2491	121	DELIGNAMGLNEQPVLVPNRAPIRAGNADELIGNAMGLLGIAYRYGGTS	STGFDCSGF
zo11_225	121	DELIGNAMGLNEQPVLVPNRAPIRAGNADELIGNAMGLLGIAYRYGGTS	STGFDCSGF
zo20_225	121	DELIGNAMGLNEQPVLVPNRAPIRAGNADELIGNAMGLLGIAYRYGGTS	STGFDCSGF
zo01_225	92	DELIGNAMGLNEQPVLVPNRAPIRAGNADELIGNAMGLLGIAYRYGGTS	STGFDCSGF
zo09_225	92	DELIGNAMGLNEQPVLVPNRAPIRAGNADELIGNAMGLLGIAYRYGGTS	STGFDCSGF
zo12_225	92	DELIGNAMGLNEQPVLVPNRAPIRAGNADELIGNAMGLLGIAYRYGGTS	STGFDCSGF
zo22_225	92	DELIGNAMGLNEQPVLVPNRAPIRAGNADELIGNAMGLLGIAYRYGGTS	STGFDCSGF
zo23_225	92	DELIGNAMGLNEQPVLVPNRAPIRAGNADELIGNAMGLLGIAYRYGGTS	STGFDCSGF
zo24_225	92	DELIGNAMGLNEQPVLVPNRAPIRAGNADELIGNAMGLLGIAYRYGGTS	STGFDCSGF
zo25_225	92	DELIGNAMGLNEQPVLVPNRAPIRAGNADELIGNAMGLLGIAYRYGGTS	STGFDCSGF
zo26_225	92	DELIGNAMGLNEQPVLVPNRAPIRAGNADELIGNAMGLLGIAYRYGGTS	STGFDCSGF
zo96_225	92	DELIGNAMGLNEQPVLVPNRAPIRAGNADELIGNAMGLLGIAYRYGGTS	STGFDCSGF
zo02_225	92	DELIGNAMGLNEQPVLVPNRAPIRAGNADELIGNAMGLLGIAYRYGGTS	STGFDCSGF
zo04_225	92	DELIGNAMGLNEQPVLVPNRAPIRAGNADELIGNAMGLLGIAYRYGGTS	STGFDCSGF
zo06_225	92	DELIGNAMGLNEQPVLVPNRAPIRAGNADELIGNAMGLLGIAYRYGGTS	STGFDCSGF
zo07_225	92	DELIGNAMGLNEQPVLVPNRAPIRAGNADELIGNAMGLLGIAYRYGGTS	STGFDCSGF
zo10_225	92	DELIGNAMGLNEQPVLVPNRAPIRAGNADELIGNAMGLLGIAYRYGGTS	STGFDCSGF
zo14_225	92	DELIGNAMGLNEQPVLVPNRAPIRAGNADELIGNAMGLLGIAYRYGGTS	STGFDCSGF
zo16_225	92	DELIGNAMGLNEQPVLVPNRAPIRAGNADELIGNAMGLLGIAYRYGGTS	STGFDCSGF
zo17_225	92	DELIGNAMGLNEQPVLVPNRAPIRAGNADELIGNAMGLLGIAYRYGGTS	STGFDCSGF
zo18_225	92	DELIGNAMGLNEQPVLVPNRAPIRAGNADELIGNAMGLLGIAYRYGGTS	STGFDCSGF
zo19_225	92	DELIGNAMGLNEQPVLVPNRAPIRAGNADELIGNAMGLLGIAYRYGGTS	STGFDCSGF
zo21_225	92	DELIGNAMGLNEQPVLVPNRAPIRAGNADELIGNAMGLLGIAYRYGGTS	STGFDCSGF
zo27_225	92	DELIGNAMGLNEQPVLVPNRAPIRAGNADELIGNAMGLLGIAYRYGGTS	STGFDCSGF
zo28_225	92	DELIGNAMGLNEQPVLVPNRAPIRAGNADELIGNAMGLLGIAYRYGGTS	STGFDCSGF
zo29_225	92	DELIGNAMGLNEQPVLVPNRAPIRAGNADELIGNAMGLLGIAYRYGGTS	STGFDCSGF
zo13_225	92	DELIGNAMGLNEQPVLVPNRAPIRAGNADELIGNAMGLLGIAYRYGGTS	STGFDCSGF
zo03_225	92	DELIGNAMGLNEQPVLVPNRAPIRAGNADELIGNAMGLLGIAYRYGGTS	STGFDCSGF
zo15_225	75	.....QPVLVPNRAPIRAGNADELIGSAMGLLGIAYRYGGTS	STGFDCSGF
fa1090	75	.....QPVLVPNRAPIRAGNADELIGSAMGLLGIAYRYGGTS	STGFDCSGF
zo32_225	75	.....QPVLVPNRAPIRAGNADELIGSAMGLLGIAYRYGGTS	STGFDCSGF
zo33_225	75	.....QPVLVPNRAPIRAGNADELIGSAMGLLGIAYRYGGTS	STGFDCSGF
zo05_225	152	MQHIFKRAMGINLPRTSQAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF	
zo08_225	152	MQHIFKRAMGINLPRTSQAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF	
z2491	181	MQHIFKRAMGINLPRTSQAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF	
zo11_225	181	MQHIFKRAMGINLPRTSQAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF	
zo20_225	181	MQHIFKRAMGINLPRTSQAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF	
zo01_225	152	MQHIFKRAMGINLPRTSQAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF	
zo09_225	152	MQHIFKRAMGINLPRTSQAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF	
zo12_225	152	MQHIFKRAMGINLPRTSQAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF	
zo22_225	152	MQHIFKRAMGINLPRTSQAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF	
zo23_225	152	MQHIFKRAMGINLPRTSQAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF	
zo24_225	152	MQHIFKRAMGINLPRTSQAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF	
zo25_225	152	MQHIFKRAMGINLPRTSQAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF	
zo26_225	152	MQHIFKRAMGINLPRTSQAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF	
zo27_225	152	MQHIFKRAMGINLPRTSQAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF	
zo28_225	152	MQHIFKRAMGINLPRTSQAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF	
zo29_225	152	MQHIFKRAMGINLPRTSQAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF	
zo13_225	152	MQHIFKRAMGINLPRTSQAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF	
zo03_225	152	MQHIFKRAMGINLPRTSQAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF	
zo15_225	123	MQHIFKRAMGINLPRTSQAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF	
fa1090	123	MQHIFKRAMGINLPRTSQAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF	
zo32_225	123	MQHIFKRAMGINLPRTSQAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF	
zo33_225	123	MQHIFKRAMGINLPRTSQAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF	

Fig. 19B

09/674546

WO 99/57280

PCT/US99/09346

20/30

zo05_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo08_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
z2491	241	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo11_225	241	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo20_225	241	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo01_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo09_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo12_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo22_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo23_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo24_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo25_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo26_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo96_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo02_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo04_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo06_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo07_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo10_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo14_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo16_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo17_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo18_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo19_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo21_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo27_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo28_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo29_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo13_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo03_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo15_225	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
fa1090	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo32_225	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo33_225	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*

Fig. 19C

Fig. 20A

gnmzq09	121	YQILDSVTTVSACARLVDSRNGKVLWSGSASIREGSNNNSGILGALVSAVVNQIANSLT
gnmzq31	121	YQILDSVTTVSACARLVDSRNGKVLWSGSASIREGSNNNSGILGALVCAVVNQIANSLT
fa1090	121	YQILDSVTTVSACARLVDSRNGKELWSGSASIREGSNNNSGILGALVCAVVNQIANSLT
gnmzq32	121	YQILDSVTTVSACARLVDSRNGKELWSGSASIREGSNNNSGILGALVCAVVNQIANSLT
gnmzq33	121	YQILDSVTTVSACARLVDSRNGKELWSGSASIREGSNNNSGILGALVCAVVNQIANSLT
gnmzq01	121	YQILDSVTTVSACARLVDSRNGKELWSGSASIREGSNNNSGILGALVSAVVNQIANSLT
gnmzq05	121	YQILDSVTTVSACARLVDSRNGKELWSGSASIREGSNNNSGILGALVSAVVNQIANSLT
gnmzq08	121	YQILDSVTTVSACARLVDSRNGKELWSGSASIREGSNNNSGILGALVSAVVNQIANSLT
gnmzq02	121	YQILDSVTTVSACARLVDSRNGKELWSGSASIREGSNNNSGILGALVSAVVNQIANSLT
gnmzq03	121	YQILDSVTTVSACARLVDSRNGKELWSGSASIREGSNNNSGILGALVSAVVNQIANSLT
gnmzq04	121	YQILDSVTTVSACARLVDSRNGKELWSGSASIREGSNNNSGILGALVSAVVNQIANSLT
gnmzq07	121	YQILDSVTTVSACARLVDSRNGKELWSGSASIREGSNNNSGILGALVSAVVNQIANSLT
gnmzq10	121	YQILDSVTTVSACARLVDSRNGKELWSGSASIREGSNNNSGILGALVSAVVNQIANSLT
gnmzq11	121	YQILDSVTTVSACARLVDSRNGKELWSGSASIREGSNNNSGILGALVSAVVNQIANSLT
gnmzq13	121	YQILDSVTTVSACARLVDSRNGKELWSGSASIREGSNNNSGILGALVSAVVNQIANSLT
gnmzq15	121	YQILDSVTTVSACARLVDSRNGKELWSGSASIREGSNNNSGILGALVSAVVNQIANSLT
gnmzq16	121	YQILDSVTTVSACARLVDSRNGKELWSGSASIREGSNNNSGILGALVSAVVNQIANSLT
gnmzq17	121	YQILDSVTTVSACARLVDSRNGKELWSGSASIREGSNNNSGILGALVSAVVNQIANSLT
gnmzq19	121	YQILDSVTTVSACARLVDSRNGKELWSGSASIREGSNNNSGILGALVSAVVNQIANSLT
gnmzq21	121	YQILDSVTTVSACARLVDSRNGKELWSGSASIREGSNNNSGILGALVSAVVNQIANSLT
gnmzq22	121	YQILDSVTTVSACARLVDSRNGKELWSGSASIREGSNNNSGILGALVSAVVNQIANSLT
gnmzq23	121	YQILDSVTTVSACARLVDSRNGKELWSGSASIREGSNNNSGILGALVSAVVNQIANSLT
gnmzq24	121	YQILDSVTTVSACARLVDSRNGKELWSGSASIREGSNNNSGILGALVSAVVNQIANSLT
gnmzq25	121	YQILDSVTTVSACARLVDSRNGKELWSGSASIREGSNNNSGILGALVSAVVNQIANSLT
gnmzq27	121	YQILDSVTTVSACARLVDSRNGKELWSGSASIREGSNNNSGILGALVSAVVNQIANSLT
gnmzq28	121	YQILDSVTTVSACARLVDSRNGKELWSGSASIREGSNNNSGILGALVSAVVNQIANSLT
gnmzq29	121	YQILDSVTTVSACARLVDSRNGKELWSGSASIREGSNNNSGILGALVSAVVNQIANSLT
z2491	121	YQILDSVTTVSACARLVDSRNGKELWSGSASIREGSNNNSGILGALVSAVVNQIANSLT
gnmzq14	121	YQILDSVTTVSACARLVDSRNGKELWSGSASIREGSNNNSGILGALVCAVVNQIANSLT
gnmzq18	121	YQILDSVTTVSACARLVDSRNGKELWSGSASIREGSNNNSGILGALVCAVVNQIANSLT
gnmzq26	121	YQILDSVTTVSACARLVDSRNGKELWSGSASIREGSNNNSGILGALVCAVVNQIANSLT
gnmzq09	181	DRGYQVSKTAAYNLLSPYSHNGIILKGPRFVEEQPK*
gnmzq31	181	DRGYQVSKTAAYNLLSPYSHNGIILKGPRFVEEQPK*
fa1090	181	DRGYQVSKTAAYNLLSPYSHNGIILKGPRFVEEQPK*
gnmzq32	181	DRGYQVSKTAAYNLLSPYSHNGIILKGPRFVEEQPK*
gnmzq33	181	DRGYQVSKTAAYNLLSPYSHNGIILKGPRFVEEQPK*
gnmzq01	181	DRGYQVSKTAAYNLLSPYSHNGIILKGPRFVEEQPK*
gnmzq05	181	DRGYQVSKTAAYNLLSPYSHNGIILKGPRFVEEQPK*
gnmzq08	181	DRGYQVSKTAAYNLLSPYSHNGIILKGPRFVEEQPK*
gnmzq02	181	DRGYQVSKTAAYNLLSPYSHNGIILKGPRFVEEQPK*
gnmzq03	181	DRGYQVSKTAAYNLLSPYSHNGIILKGPRFVEEQPK*
gnmzq04	181	DRGYQVSKTAAYNLLSPYSHNGIILKGPRFVEEQPK*
gnmzq07	181	DRGYQVSKTAAYNLLSPYSHNGIILKGPRFVEEQPK*
gnmzq10	181	DRGYQVSKTAAYNLLSPYSHNGIILKGPRFVEEQPK*
gnmzq11	181	DRGYQVSKTAAYNLLSPYSHNGIILKGPRFVEEQPK*
gnmzq13	181	DRGYQVSKTAAYNLLSPYSHNGIILKGPRFVEEQPK*
gnmzq15	181	DRGYQVSKTAAYNLLSPYSHNGIILKGPRFVEEQPK*
gnmzq16	181	DRGYQVSKTAAYNLLSPYSHNGIILKGPRFVEEQPK*
gnmzq17	181	DRGYQVSKTAAYNLLSPYSHNGIILKGPRFVEEQPK*
gnmzq19	181	DRGYQVSKTAAYNLLSPYSHNGIILKGPRFVEEQPK*
gnmzq21	181	DRGYQVSKTAAYNLLSPYSHNGIILKGPRFVEEQPK*
gnmzq22	181	DRGYQVSKTAAYNLLSPYSHNGIILKGPRFVEEQPK*
gnmzq23	181	DRGYQVSKTAAYNLLSPYSHNGIILKGPRFVEEQPK*
gnmzq24	181	DRGYQVSKTAAYNLLSPYSHNGIILKGPRFVEEQPK*
gnmzq25	181	DRGYQVSKTAAYNLLSPYSHNGIILKGPRFVEEQPK*
gnmzq27	181	DRGYQVSKTAAYNLLSPYSHNGIILKGPRFVEEQPK*
gnmzq28	181	DRGYQVSKTAAYNLLSPYSHNGIILKGPRFVEEQPK*
gnmzq29	181	DRGYQVSKTAAYNLLSPYSHNGIILKGPRFVEEQPK*
z2491	181	DRGYQVSKTAAYNLLSPYSHNGIILKGPRFVEEQPK*
gnmzq14	181	DRGYQVSKTAAYNLLSPYSHNGIILKGPRFVEEQPK*
gnmzq18	181	DRGYQVSKTAAYNLLSPYSHNGIILKGPRFVEEQPK*
gnmzq26	181	DRGYQVSKTAAYNLLSPYSHNGIILKGPRFVEEQPK*

Fig. 20B

287_14	1	MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSKPAAPVV <del>SE</del> KE TEA
287_2	1	MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSKPAAPVV <del>SE</del> KE TEA
287_21	1	MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSKPAAPVV <del>SE</del> KE TEA
z2491	1	MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSKPAAPVV <del>SE</del> KE TEA
287_9	1	MFKRSVIAMACIVALSACGGGGGGSPDVKSADTLSKPAAPVV <del>EDVGEEVLPEKKDDEEA</del>
fa1090	1	MFKRSVIAMACIFPLSACGGGGGGSPDVKSADTPSKPAAPVV <del>ENAGEGVLPKEKKDDEEA</del>
287_14	50	KEDAPQAGSQGQGAPSQGQDMAAVSEENTNGGAAATDKPKNEDEGAQNDMPQNAADT
287_2	50	KEDAPQAGSQGQGAPSQGQDMAAVSEENTNGGAAATDKPKNEDEGAQNDMPQNAADT
287_21	50	KEDAPQAGSQGQGAPSXQGSQDMAAVSEENTNGGAAVTADNPKNEDEVQAQNDMPQNAAGT
z2491	50	KEDAPQAGSQGQGAPSQGQDMAAVSEENTNGGAAVTADNPKNEDEVQAQNDMPQNAAGT
287_9	61	VSGAPQADT <del>QD</del> ATAGKGGDMAAVSAENTNGGAA <del>AT</del> TDNPENKDEGPQNDMPQNAADT
fa1090	61	AGGAPQADT <del>QD</del> ATAGE <del>G</del> SQDMAAVSAENTNGGAA <del>AT</del> TDNPKNEDAGAQNDMPQNAADT
287_14	110	DSLTPNHTPASNMPAGNME <del>NOA</del> DAGESEQPANQPD <del>MAN</del> ADGMQGDDPSAGGENAGNTA
287_2	110	DSLTPNHTPASNMPAGNME <del>NOA</del> DAGESEQPANQPD <del>MAN</del> ADGMQGDDPSAGGENAGNTA
287_21	110	DSSTPNHTPDPNMLAGNME <del>NOA</del> DAGES <del>S</del> OPANQPD <del>MAN</del> ADGMQGDDPSAGGENAGNTA
z2491	110	DSSTPNHTPDPNMLAGNME <del>NOA</del> DAGES <del>S</del> OPANQPD <del>MAN</del> ADGMQGDDPSAGGENAGNTA
287_9	119	DSSTPNHTPAPNMPTRDMGNQADAGES <del>S</del> OPANQPD <del>MAN</del> ADGMQGDDPSAGGENAGNTA
fa1090	117	.....
287_14	170	AQ <del>C</del> TNOAENNO <del>T</del> AGSQN <del>P</del> ASS <del>T</del> NPSATNSCGDFGR <del>T</del> NCNSV <del>A</del> IDGPSQNITLTHCKGDS
287_2	170	AQ <del>C</del> TNOAENNO <del>T</del> AGSQN <del>P</del> ASS <del>T</del> NPSATNSCGDFGR <del>T</del> NCNSV <del>A</del> IDGPSQNITLTHCKGDS
287_21	170	AQ <del>C</del> ANQAGNNQ <del>A</del> AGSSDPIPASNP <del>A</del> PANGCSM <del>F</del> GRV <del>D</del> INGV <del>A</del> IDGPSQNITLTHCKGDS
z2491	170	AQ <del>C</del> ANQAGNNQ <del>A</del> AGSSDPIPASNP <del>A</del> PANGCSM <del>F</del> GRV <del>D</del> INGV <del>A</del> IDGPSQNITLTHCKGDS
287_9	178	D <del>Q</del> ANQAE <del>N</del> NQ <del>V</del> CGSQN <del>P</del> ASS <del>T</del> N <del>A</del> TNGGSD <del>F</del> GRINV <del>A</del> NGE <del>K</del> EDSG <del>S</del> EN <del>V</del> TLTHCKD <del>K</del> V
fa1090	117	ESANQ <del>T</del> GNNQ <del>P</del> AGSSD <del>S</del> APASNP <del>A</del> PANGCS <del>D</del> GR <del>T</del> NCNSV <del>A</del> IDGPSQNITLTHCKGDS
287_14	230	CSGNNFLDEEVQLKSEFEKLS <del>D</del> AK <del>I</del> S <del>N</del> YKKDGKNDGK <del>N</del> IKFVGLVADSVQMKG <del>I</del> NOX <del>II</del>
287_2	230	CSGNNFLDEEVQLKSEFEKLS <del>D</del> AK <del>I</del> S <del>N</del> YKKDGKNDGK <del>N</del> IKFVGLVADSVQMKG <del>I</del> NOX <del>II</del>
287_21	230	CSGNNFLDEEVQLKSEFEKLS <del>D</del> AK <del>I</del> S <del>N</del> YKK <del>...</del> DGKNDK <del>F</del> VGLVADSVQMKG <del>I</del> NOX <del>II</del>
z2491	230	CSGNNFLDEEVQLKSEFEKLS <del>D</del> AK <del>I</del> S <del>N</del> YKK <del>...</del> DGKNDK <del>F</del> VGLVADSVQMKG <del>I</del> NOX <del>II</del>
287_9	238	CDRD <del>F</del> LDEEAPPKSEFEKLS <del>D</del> AK <del>I</del> KINKYKK <del>...</del> DEQR <del>E</del> NFVGLVADRV <del>E</del> KNG <del>T</del> NKY <del>II</del>
fa1090	176	CNGDN <del>N</del> LLDEEAPS <del>K</del> SEFEKLS <del>D</del> AK <del>I</del> KIKRYKK <del>...</del> DEQR <del>E</del> NFVGLVADRVKKDGT <del>N</del> KY <del>II</del>
287_14	290	FYKPKP <del>...</del> TSFARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEG
287_2	290	FYKPKP <del>...</del> TSFARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEG
287_21	286	FYKPKP <del>...</del> TSFARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEG
z2491	286	FYKPKP <del>...</del> TSFARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEG
287_9	293	IYKD <del>K</del> SASS <del>S</del> ARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEG
fa1090	232	FYTDKPK <del>...</del> RSAR <del>S</del> RRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEG
287_14	348	NYRYLTYGAEKLPGGSYALRVQ <del>G</del> EP <del>S</del> KGEM <del>I</del> LAG <del>A</del> VYNGEV <del>L</del> H <del>F</del> ENGRPS <del>P</del> GR <del>F</del> AA
287_2	348	NYRYLTYGAEKLPGGSYALRVQ <del>G</del> EP <del>S</del> KGEM <del>I</del> LAG <del>A</del> VYNGEV <del>L</del> H <del>F</del> ENGRPS <del>P</del> GR <del>F</del> AA
287_21	344	NYRYLTYGAEKLPGGSYALRVQ <del>G</del> EP <del>S</del> KGEM <del>I</del> LAG <del>A</del> VYNGEV <del>L</del> H <del>F</del> ENGRPV <del>P</del> GR <del>F</del> AA
z2491	344	NYRYLTYGAEKLPGGSYALRVQ <del>G</del> EP <del>S</del> KGEM <del>I</del> LAG <del>A</del> VYNGEV <del>L</del> H <del>F</del> ENGRPV <del>P</del> GR <del>F</del> AA
287_9	353	NYRYLTYGAEKLPGGSYALRVQ <del>G</del> EP <del>S</del> KGEM <del>I</del> LAG <del>A</del> VYNGEV <del>L</del> H <del>F</del> ENGRPS <del>P</del> GR <del>F</del> AA
fa1090	285	NYRYLTYGAEKLPGGSYALRVQ <del>G</del> EP <del>S</del> KGEM <del>I</del> LAG <del>A</del> VYNGEV <del>L</del> H <del>F</del> ENGRPV <del>P</del> GR <del>F</del> AA
287_14	408	KVDFGSKSVDGI <del>I</del> D <del>S</del> GD <del>L</del> HMGTQKF <del>K</del> AAIDGNGFKGTWTENG <del>G</del> GDVSG <del>G</del> FYGPAGEEVA
287_2	408	KVDFGSKSVDGI <del>I</del> D <del>S</del> GD <del>L</del> HMGTQKF <del>K</del> AAIDGNGFKGTWTENG <del>G</del> GDVSG <del>G</del> FYGPAGEEVA
287_21	404	KVDFGSKSVDGI <del>I</del> D <del>S</del> GD <del>L</del> HMGTQKF <del>K</del> AAIDGNGFKGTWTENG <del>G</del> GDVSG <del>G</del> FYGPAGEEVA
z2491	404	KVDFGSKSVDGI <del>I</del> D <del>S</del> GD <del>L</del> HMGTQKF <del>K</del> AAIDGNGFKGTWTENG <del>G</del> GDVSG <del>G</del> FYGPAGEEVA
287_9	413	KVDFGSKSVDGI <del>I</del> D <del>S</del> GD <del>L</del> HMGTQKF <del>K</del> AAIDGNGFKGTWTENG <del>G</del> GDVSG <del>G</del> FYGPAGEEVA
fa1090	345	KVDFGSKSVDGI <del>I</del> D <del>S</del> GD <del>L</del> HMGTQKF <del>K</del> AAIDGNGFKGTWTENG <del>G</del> GDVSG <del>G</del> FYGPAGEEVA

FIG. 21A

09/674546

WO 99/57280

24/30

PCT/US99/09346

287_14	468	GKYSYRPTDAEKGGFGVFA	GKKEQD
287_2	468	GKYSYRPTDAEKGGFGVFA	GKKEQD
287_21	464	GKYSYRPTDAEKGGFGVFA	GKKEQD
z2491	464	GKYSYRPTDAEKGGFGVFA	GKKEQD
287_9	473	GKYSYRPTDAEKGGFGVFA	GKKEQD
fa1090	405	GKYSYRPTDAEKGGFGVFA	GKKEQD

FIG. 21B

z2491_519	61	KEIPLDVPSQVCITRDNTQLTVGDIIYFQVTDPKLASGSSNYIMAITQLAQTTLRSVIG
zv26_519	61	KEIPLDVPSQVCITRDNTQLTVGDIIYFQVTDPKLASGSSNYIMAITQLAQTTLRSVIG
zv22_519ass	61	KEIPLDVPSQVCITRDNTQLTVGDIIYFQVTDPKLASGSSNYIMAITQLAQTTLRSVIG
_<1090_519	61	KEIPLDVPSQVCITRDNTQLTVGDIIYFQVTDPKLASGSSNYIMAITQLAQTTLRSVIG
zv32_519	61	KEIPLDVPSQVCITRDNTQLTVGDIIYFQVTDPKLASGSSNYIMAITQLAQTTLRSVIG
zv11_519	61	KEIPLDVPSQVCITRDNTQLTVGDIIYFQVTDPKLASGSSNYIMAITQLAQTTLRSVIG
zv28_519	61	KEIPLDVPSQVCITRDNTQLTVGDIIYFQVTDPKLASGSSNYIMAITQLAQTTLRSVIG
zv96_519	61	KEIPLDVPSQVCITRDNTQLTVGDIIYFQVTDPKLASGSSNYIMAITQLAQTTLRSVIG
zv02_519	61	KEIPLDVPSQVCITRDNTQLTVGDIIYFQVTDPKLASGSSNYIMAITQLAQTTLRSVIG
zv03_519	61	KEIPLDVPSQVCITRDNTQLTVGDIIYFQVTDPKLASGSSNYIMAITQLAQTTLRSVIG
zv04_519	61	KEIPLDVPSQVCITRDNTQLTVGDIIYFQVTDPKLASGSSNYIMAITQLAQTTLRSVIG
zv05_519	61	KEIPLDVPSQVCITRDNTQLTVGDIIYFQVTDPKLASGSSNYIMAITQLAQTTLRSVIG
zv01_519	61	KEIPLDVPSQVCITRDNTQLTVGDIIYFQVTDPKLASGSSNYIMAITQLAQTTLRSVIG
zv07_519	61	KEIPLDVPSQVCITRDNTQLTVGDIIYFQVTDPKLASGSSNYIMAITQLAQTTLRSVIG
zv12_519	61	KEIPLDVPSQVCITRDNTQLTVGDIIYFQVTDPKLASGSSNYIMAITQLAQTTLRSVIG
zv18_519	61	KEIPLDVPSQVCITRDNTQLTVGDIIYFQVTDPKLASGSSNYIMAITQLAQTTLRSVIG
zv19_519	61	KEIPLDVPSQVCITRDNTQLTVGDIIYFQVTDPKLASGSSNYIMAITQLAQTTLRSVIG
zv21_519ass	61	KEIPLDVPSQVCITRDNTQLTVGDIIYFQVTDPKLASGSSNYIMAITQLAQTTLRSVIG
zv27_519	61	KEIPLDVPSQVCITRDNTQLTVGDIIYFQVTDPKLASGSSNYIMAITQLAQTTLRSVIG
zv20_519ass	61	KEIPLDVPSQVCITRDNTQLTVGDIIYFQVTDPKLASGSSNYIMAITQLAQTTLRSVIG
zv06_519ass	61	KEIPLDVPSQVCITRDNTQLTVGDIIYFQVTDPKLASGSSNYIMAITQLAQTTLRSVIG
zv29_519ass	61	KEIPLDVPSQVCITRDNTQLTVGDIIYFQVTDPKLASGSSNYIMAITQLAQTTLRSVIG

z2491_519	121	RMELDKTFEERDEINSTVV <del>S</del> ALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv26_519	121	RMELDKTFEERDEINSTVV <del>S</del> ALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv22_519ass	121	RMELDKTFEERDEINSTVV <del>S</del> ALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
fa1090_519	121	RMELDKTFEERDEINSTVV <del>S</del> ALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv32_519	121	RMELDKTFEERDEINSTVV <del>S</del> ALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv11_519	121	RMELDKTFEERDEINSTVV <del>S</del> ALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv28_519	121	RMELDKTFEERDEINSTVV <del>S</del> ALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv96_519	121	RMELDKTFEERDEINSTVV <del>S</del> ALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv02_519	121	RMELDKTFEERDEINSTVV <del>S</del> ALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv03_519	121	RMELDKTFEERDEINSTVV <del>S</del> ALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv04_519	121	RMELDKTFEERDEINSTVV <del>S</del> ALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv05_519	121	RMELDKTFEERDEINSTVV <del>S</del> ALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv01_519	121	RMELDKTFEERDEINSTVV <del>S</del> ALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv07_519	121	RMELDKTFEERDEINSTVV <del>S</del> ALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv12_519	121	RMELDKTFEERDEINSTVV <del>S</del> ALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv18_519	121	RMELDKTFEERDEINSTVV <del>S</del> ALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv19_519	121	RMELDKTFEERDEINSTVV <del>S</del> ALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv21_519ass	121	RMELDKTFEERDEINSTVV <del>S</del> ALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv27_519	121	RMELDKTFEERDEINSTVV <del>S</del> ALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv20_519ass	121	RMELDKTFEERDEINSTVV <del>S</del> ALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv06_519ass	121	RMELDKTFEERDEINSTVV <del>S</del> ALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv29_519ass	121	RMELDKTFEERDEINSTVV <del>S</del> ALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE

FIG. 22A

z2491_519	181	KRARIAESEGRKIEQINLASGOREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv26_519	181	KRARIAESEGRKIEQINLASGOREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv22_519ass	181	KRARIAESEGRKIEQINLASGOREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
fa1090_519	181	KRARIAESEGRKIEQINLASGOREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv32_519	181	KRARIAESEGRKIEQINLASGOREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv11_519	181	KRARIAESEGRKIEQINLASGOREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv28_519	181	KRARIAESEGRKIEQINLASGOREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv96_519	181	KRARIAESEGRKIEQINLASGOREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv02_519	181	KRARIAESEGRKIEQINLASGOREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv03_519	181	KRARIAESEGRKIEQINLASGOREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv04_519	181	KRARIAESEGRKIEQINLASGOREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv05_519	181	KRARIAESEGRKIEQINLASGOREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv01_519	181	KRARIAESEGRKIEQINLASGOREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv07_519	181	KRARIAESEGRKIEQINLASGOREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv12_519	181	KRARIAESEGRKIEQINLASGOREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv18_519	181	KRARIAESEGRKIEQINLASGOREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv19_519	181	KRARIAESEGRKIEQINLASGOREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv21_519ass	181	KRARIAESEGRKIEQINLASGOREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv27_519	181	KRARIAESEGRKIEQINLASGOREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv20_519ass	181	KRARIAESEGRKIEQINLASGOREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv06_519ass	181	KRARIAESEGRKIEQINLASGOREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv29_519ass	181	KRARIAESEGRKIEQINLASGOREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR

z2491_519	241	LVAEANAEAIRQIAAAALQTQGGGADAVNLKIAEQYVAAFFNNLAKESNTLIMPANVADIGSL
zv26_519	241	LVAEANAEAIRQIAAAALQTQGGGADAVNLKIAEQYVAAFFNNLAKESNTLIMPANVADIGSL
zv22_519ass	241	LVAEANAEAIRQIAAAALQTQGGGADAVNLKIAEQYVAAFFNNLAKESNTLIMPANVADIGSL
fa1090_519	241	LVAEANAEAIRQIAAAALQTQGGGADAVNLKIAEQYVAAFFNNLAKESNTLIMPANVADIGSL
zv32_519	241	LVAEANAEAIRQIAAAALQTQGGGADAVNLKIAEQYVAAFFNNLAKESNTLIMPANVADIGSL
zv11_519	241	LVAEANAEAIRQIAAAALQTQGGGADAVNLKIAEQYVAAFFNNLAKESNTLIMPANVADIGSL
zv28_519	241	LVAEANAEAIRQIAAAALQTQGGGADAVNLKIAEQYVAAFFNNLAKESNTLIMPANVADIGSL
zv96_519	241	LVAEANAEAIRQIAAAALQTQGGGADAVNLKIAEQYVAAFFNNLAKESNTLIMPANVADIGSL
zv02_519	241	LVAEANAEAIRQIAAAALQTQGGGADAVNLKIAEQYVAAFFNNLAKESNTLIMPANVADIGSL
zv03_519	241	LVAEANAEAIRQIAAAALQTQGGGADAVNLKIAEQYVAAFFNNLAKESNTLIMPANVADIGSL
zv04_519	241	LVAEANAEAIRQIAAAALQTQGGGADAVNLKIAEQYVAAFFNNLAKESNTLIMPANVADIGSL
zv05_519	241	LVAEANAEAIRQIAAAALQTQGGGADAVNLKIAEQYVAAFFNNLAKESNTLIMPANVADIGSL
zv01_519	241	LVAEANAEAIRQIAAAALQTQGGGADAVNLKIAEQYVAAFFNNLAKESNTLIMPANVADIGSL
zv07_519	241	LVAEANAEAIRQIAAAALQTQGGGADAVNLKIAEQYVAAFFNNLAKESNTLIMPANVADIGSL
zv12_519	241	LVAEANAEAIRQIAAAALQTQGGGADAVNLKIAEQYVAAFFNNLAKESNTLIMPANVADIGSL
zv18_519	241	LVAEANAEAIRQIAAAALQTQGGGADAVNLKIAEQYVAAFFNNLAKESNTLIMPANVADIGSL
zv19_519	241	LVAEANAEAIRQIAAAALQTQGGGADAVNLKIAEQYVAAFFNNLAKESNTLIMPANVADIGSL
zv21_519ass	241	LVAEANAEAIRQIAAAALQTQGGGADAVNLKIAEQYVAAFFNNLAKESNTLIMPANVADIGSL
zv27_519	241	LVAEANAEAIRQIAAAALQTQGGGADAVNLKIAEQYVAAFFNNLAKESNTLIMPANVADIGSL
zv20_519ass	241	LVAEANAEAIRQIAAAALQTQGGGADAVNLKIAEQYVAAFFNNLAKESNTLIMPANVADIGSL
zv06_519ass	241	LVAEANAEAIRQIAAAALQTQGGGADAVNLKIAEQYVAAFFNNLAKESNTLIMPANVADIGSL
zv29_519ass	241	LVAEANAEAIRQIAAAALQTQGGGADAVNLKIAEQYVAAFFNNLAKESNTLIMPANVADIGSL

z2491_519	301	ISAGMKIIDSSKTAK*
zv26_519	301	ISAGMKIIDSSKTAK*
zv22_519ass	301	ISAGMKIIDSSKTAK*
fa1090_519	301	ISAGMKIIDSSKTAK*
zv32_519	301	ISAGMKIIDSSKTAK*
zv11_519	301	ISAGMKIIDSSKTAK*
zv28_519	301	ISAGMKIIDSSKTAK*
zv96_519	301	ISAGMKIIDSSKTAK*
zv02_519	301	ISAGMKIIDSSKTAK*
zv03_519	301	ISAGMKIIDSSKTAK*
zv04_519	301	ISAGMKIIDSSKTAK*
zv05_519	301	ISAGMKIIDSSKTAK*
zv01_519	301	ISAGMKIIDSSKTAK*
zv07_519	301	ISAGMKIIDSSKTAK*
zv12_519	301	ISAGMKIIDSSKTAK*
zv18_519	301	ISAGMKIIDSSKTAK*
zv19_519	301	ISAGMKIIDSSKTAK*
zv21_519ass	301	ISAGMKIIDSSKTAK*
zv27_519	301	ISAGMKIIDSSKTAK*
zv20_519ass	301	ISAGMKIIDSSKTAK*
zv06_519ass	301	ISAGMKIIDSSKTAK*
zv29_519ass	301	ISAGMKIIDSSKTAK*

Fig. 22B

Fig. 23A

fa1090	121	YFTPWQVAGNGSLAGTVTGYEYEPVULKGDGRTERARFPPIYGIPDDFISVPLPAGLRRGKNA z...3asbc
zm32asbc	121	YFTPWQVAGNGSLAGTVTGYEYEPVULKGDGRTERARFPPIYGIPDDFISVPLPAGLRRGKNA zm23asbc
zm27bc	121	YFTPWQVAGNGSLAGTVTGYEYEPVULKGDGRRTAQARFPPIYGIPDDFISVPLPAGLRSGKA zm09
zm10	121	YFTPWQVAGNGSLAGTVTGYEYEPVULKGDGRRTAQARFPPIYGIPDDFISVPLPAGLRSGKA zm24
zm25	121	YFTPWQVAGNGSLAGTVTGYEYEPVULKGDGRRTAQARFPPIYGIPDDFISVPLPAGLRSGKA zm14
zm04	121	YFTPWQVAGNGSLAGTVTGYEYEPVULKGDGRRTAQARFPPIYGIPDDFISVPLPAGLRSGKA zm11asbc
zm08n	121	YFTPWQVAGNGSLAGTVTGYEYEPVULKGDGRRTAQARFPPIYGIPDDFISVPLPAGLRSGKA zm96
zm01	121	YFTPWQVAGNGSLAGTVTGYEYEPVULKGDGRRTAQARFPPIYGIPDDFISVPLPAGLRSGKA zm02
zm03	121	YFTPWQVAGNGSLAGTVTGYEYEPVULKGDGRRTAQARFPPIYGIPDDFISVPLPAGLRSGKA zm07
zm12	121	YFTPWQVAGNGSLAGTVTGYEYEPVULKGDGRRTAQARFPPIYGIPDDFISVPLPAGLRSGKA zm18
zm19	121	YFTPWQVAGNGSLAGTVTGYEYEPVULKGDGRRTAQARFPPIYGIPDDFISVPLPAGLRSGKA zm20
zm21	121	YFTPWQVAGNGSLAGTVTGYEYEPVULKGDGRRTAQARFPPIYGIPDDFISVPLPAGLRSGKA zm06
zm17	121	YFTPWQVAGNGSLAGTVTGYEYEPVULKGDGRRTAQARFPPIYGIPDDFISVPLPAGLRSGKA zm13
zm05	121	YFTPWQVAGNGSLAGTVTGYEYEPVULKGDGRRTAQARFPPIYGIPDDFISVPLPAGLRSGKA z2491
zm22	121	YFTPWQVAGNGSLAGTVTGYEYEPVULKGDGRRTAQARFPPIYGIPDDFISVPLPAGLRSGKA zm26
zm28	121	YFTPWQVAGNGSLAGTVTGYEYEPVULKGDGRRTAQARFPPIYGIPDDFISVPLPAGLRSGKA zm29asbc
zm16	121	YFTPWQVAGNGSLAGTVTGYEYEPVULKGDGRRTAQARFPPIYGIPDDFISVPLPAGLRSGKA zm15
zm31asbc	121	YFTPWQVAGNGSLAGTVTGYEYEPVULKGDGRRTAQARFPPIYGIPDDFISVPLPAGLRSGKA fa1090
zm33asbc	181	LVRIRQTGKNSGTTIDNAGGHTADLSRFPIARTATAIKGRFEGSRFLPYHTRNQINGGAL zm32asbc
zm23asbc	181	LVRIRQTGKNSGTTIDNAGGHTADLSRFPIARTATAIKGRFEGSRFLPYHTRNQINGGAL zm27bc
zm09	181	LVRIRQTGKNSGTTIDNTGGHTADLSRFPIARTATAIKGRFEGSRFLPYHTRNQINGGAL zm10
zm24	181	LVRIRQTGKNSGTTIDNTGGHTADLSRFPIARTATAIKGRFEGSRFLPYHTRNQINGGAL zm25
zm14	181	LVRIRQTGKNSGTTIDNTGGHTADLSRFPIARTATAIKGRFEGSRFLPYHTRNQINGGAL zm04
zm11asbc	181	LVRIRQTGKNSGTTIDNTGGHTADLSRFPIARTATAIKGRFEGSRFLPYHTRNQINGGAL zm08n
zm96	181	LVRIRQTGKNSGTTIDNTGGHTADLSRFPIARTATAIKGRFEGSRFLPYHTRNQINGGAL zm01
zm02	181	LVRIRQTGKNSGTTIDNTGGHTADLSRFPIARTATAIKGRFEGSRFLPYHTRNQINGGAL zm03
zm07	181	LVRIRQTGKNSGTTIDNTGGHTADLSRFPIARTATAIKGRFEGSRFLPYHTRNQINGGAL zm12
zm18	181	LVRIRQTGKNSGTTIDNTGGHTADLSRFPIARTATAIKGRFEGSRFLPYHTRNQINGGAL zm19
zm20	181	LVRIRQTGKNSGTTIDNTGGHTADLSRFPIARTATAIKGRFEGSRFLPYHTRNQINGGAL zm21
zm06	181	LVRIRQTGKNSGTTIDNTGGHTADLSRFPIARTATAIKGRFEGSRFLPYHTRNQINGGAL zm17
zm13	181	LVRIRQTGKNSGTTIDNTGGHTADLSRFPIARTATAIKGRFEGSRFLPYHTRNQINGGAL zm05
z2491	181	LVRIRQTGKNSGTTIDNTGGHTADLSRFPIARTATAIKGRFEGSRFLPYHTRNQINGGAL zm22
zm26	181	LVRIRQTGKNSGTTIDNTGGHTADLSRFPIARTATAIKGRFEGSRFLPYHTRNQINGGAL zm28
zm29asbc	181	LVRIRQTGKNSGTTIDNTGGHTADLSRFPIARTATAIKGRFEGSRFLPYHTRNQINGGAL zm16
zm15	181	LVRIRQTGKNSGTTIDNTGGHTADLSRFPIARTATAIKGRFEGSRFLPYHTRNQINGGAL zm31asbc

Fig. 23B

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29/30

Fig. 23C

fa1090	361	1DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm33asbc	361	1DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm32asbc	361	1DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm23asbc	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm27bc	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm09	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm10	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm24	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm25	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm14	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm04	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm11asbc	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm08n	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm96	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm01	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm02	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm03	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm07	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm12	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm18	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm19	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm20	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm21	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm06	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm17	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm13	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm05	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
z2491	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm22	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm26	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm28	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm29asbc	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm16	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm15	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
zm31asbc	361	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
fa1090	421	QKTTGYVWQLLPNGMMPKEYRP*
zm33asbc	421	QKTTGYVWQLLPNGMMPKEYRP*
zm32asbc	421	QKTTGYVWQLLPNGMMPKEYRP*
zm23asbc	421	MKEPGYVWQLLPNGMMPKEYRP*
zm27bc	421	MKEPGYVWQLLPNGMMPKEYRP*
zm09	421	QKTTGYVWQLLPNGMMPKEYRP*
zm10	421	QKTTGYVWQLLPNGMMPKEYRP*
zm24	421	QKTTGYVWQLLPNGMMPKEYRP*
zm25	421	QKTTGYVWQLLPNGMMPKEYRP*
zm14	421	QKTTGYVWQLLPNGMMPKEYRP*
zm04	421	QKTTGYVWQLLPNGMMPKEYRP*
zm11asbc	421	QKTTGYVWQLLPNGMMPKEYRP*
zm08n	421	QKTTGYVWQLLPNGMMPKEYRP*
zm96	421	QKTTGYVWQLLPNGMMPKEYRP*
zm01	421	QKTTGYVWQLLPNGMMPKEYRP*
zm02	421	QKTTGYVWQLLPNGMMPKEYRP*
zm03	421	QKTTGYVWQLLPNGMMPKEYRP*
zm07	421	QKTTGYVWQLLPNGMMPKEYRP*
zm12	421	QKTTGYVWQLLPNGMMPKEYRP*
zm18	421	QKTTGYVWQLLPNGMMPKEYRP*
zm19	421	QKTTGYVWQLLPNGMMPKEYRP*
zm20	421	QKTTGYVWQLLPNGMMPKEYRP*
zm21	421	QKTTGYVWQLLPNGMMPKEYRP*
zm06	421	QKTTGYVWQLLPNGMMPKEYRP*
zm17	421	QKTTGYVWQLLPNGMMPKEYRP*
zm13	421	QKTTGYVWQLLPNGMMPKEYRP*
zm05	421	QKTTGYVWQLLPNGMMPKEYRP*
z2491	421	QKTTGYVWQLLPNGMMPKEYRP*
zm22	421	QKTTGYVWQLLPNGMMPKEYRP*
zm26	421	QKTTGYVWQLLPNGMMPKEYRP*
zm28	421	QKTTGYVWQLLPNGMMPKEYRP*
zm29asbc	421	QKTTGYVWQLLPNGMMPKEYRP*
zm16	421	QKTTGYVWQLLPNGMMPKEYRP*
zm15	421	QKTTGYVWQLLPNGMMPKEYRP*
zm31asbc	421	QKTTGYVWQLLPNGMMPKEYRP*

Fig. 23D